

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 13, 2002, 06:42:55 ; Search time 2040.31 Seconds
(without alignments)
13897.622 Million cell updates/sec

Title: US-09-664-840-1

Perfect score: 1355
Sequence: 1 gcttgagactctctctac.....ttgtgtcaaaaaaaaaa 1355

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenBml: *
1: gb_da: *
2: gb_htg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *
15: em_da: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_vl: *
30: em_htg_hum: *
31: em_htg_inv: *
32: em_htg_other: *
33: em_htgo_inv: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
1	1337.4	98.7	1358	AF247133
2	351.6	25.9	1346	AY050838
3	286	21.1	8	AF332433
4	286	21.1	8	D88536
5	284.8	21.0	8	D88537
6	284.8	21.0	8	AY045918
7	265.2	19.6	900	AF332434
8	261.6	19.3	8	D49384
9	260	19.2	8	D49385
10	260	19.2	8	S80863
11	260	19.2	8	D49383
12	242	17.9	900	AF332427
13	189.4	14.0	819	T46889
14	189.4	14.0	23	E09606
15	189.4	14.0	819	E11367
16	189.4	14.0	2618	ANADESCA
17	159.8	11.8	1464	SPAJ2065
18	158.8	11.7	957	T46888
19	158.8	11.7	957	E11367
20	158.8	11.7	1275	SYCDSE9
21	158.8	11.7	113064	SYCDSE9
22	130	9.6	1068	SVU90417
23	127.8	9.4	342800	AP003598
24	115.2	8.5	2784	SPU36390
25	102.2	7.5	837	ANDSG
26	102.2	7.5	837	E64527
27	100	7.4	81370	AB017071
28	90.6	6.7	74316	T21E18
29	90.6	6.7	95600	AC024227
30	87	6.4	50785	AC007169
31	81.2	6.0	41039	T2D23
32	72.6	5.4	366	AF002252
33	68	5.0	2404	AF272343
34	64.2	4.7	1307	D83478
35	60	4.4	3371	AB024576
36	59.8	4.4	2059	CCARCOFE1
37	58.4	4.3	1883	AB037570
38	58.2	4.3	1020	AF260244
39	58.2	4.3	1020	AX338586
40	57.6	4.3	1316	D84474
41	57.4	4.2	1423	AF272345
42	57.4	4.2	2251	E15491
43	57.4	4.2	2251	D83185
44	57.4	4.2	22448	PFMAL4P4
45	57.2	4.2	1017	AF260243

ALIGNMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	TITLE	JOURNAL	MEDLINE	PUBMED	REFERENCE	AUTHORS	TITLE
1	AF247133	Limnanthes douglasii delta5 acyl-CoA desaturase mRNA, partial cds.	AF247133	1	GI:11066474	Douglas's meadowfoam.	Limnanthes douglasii	1358 bp mRNA linear, PLN 02-NOV-2000						
	AF247133	Limnanthes douglasii delta5 acyl-CoA desaturase mRNA, partial cds.	AF247133	1	GI:11066474	Douglas's meadowfoam.	Limnanthes douglasii	1358 bp mRNA linear, PLN 02-NOV-2000						
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[illegible]

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D	721	TACTTTACTACGTCCGAGGGTTCCATACATTTGCTCGGGAAATGGSTTTAAGTTGGTAT	780
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D	781	TTATGTTCATTTCACACTTTCGGTATCAACTAGTTTGCTATAAATGGGCGGAAGGCCAT	840
OY	841	ggaatactgagaatttatcgcaccaacaatatgtttgtgcattgtgtcgttttggaag	900
D	841	GGAATACTGGAATTATATGACCACAATAATATTGTGTCATTGCTGGTGTGAGAGCG	900
OY	901	gcttgcataacacccccacgccattcgaacaatgatgcgtcacacgggctcagaattgtagc	960
D	901	GCTGCGATACACACCAACCGCATTCGAAACAATCAGCTGACACGGGCTAGAAATGGTGG	960
OY	961	agatcgatgttacttgttacgttatacaggacctcaaaagctattgattgtctaccatg	1020
D	961	AGATCGATGTACTTGTGTACGTATTACAGGACGCTCAACACTTTGGATTGGCTACCAANG	1020
OY	1021	tgaagctaccaaactgaagctcagaagcaaaagctcaaaagcagtgccaagaagttt	1080
D	1021	TGAAGCTACCAACTGAAGCTCAGAAGCAAAAAGCTCAAAAGCAAGAGTGCCCTAAGAGATT	1080
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D	1081	GAAAGATGTAATAAAGTGTGTATTGATGATCACTAATTATATATGTTTTCAAGAGCTGATCG	1140
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D	1141	TGTAAATGAATAAAGTTCGAGGCGACGATATATACAGTGTGCGAATATGAATAATCGTTTGA	1200
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D	1201	TTTTTGTATCTGATCGAATAAATAGTCGCCCTGTATAGGTGTTCATGTAAACATTTGATGTT	1260
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D	1261	GTTTGTGTGATGTTGTGTGGGCTTCTCTTTGATGCTGATATGTTGTGTGTGCACGTTTGGAGA	1320
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LOCUS		Arabidopsis thaliana putative delta p desaturase	
DEFINITION		(MSJL_25/Atg15850) mRNA, complete cds.	
ACCESSION		AY050838	
VERSION		AY050838.1 GI:15292808	
KEYWORDS		FLI CDNA.	
SOURCE		thale cress.	
ORGANISM		Arabidopsis thaliana	
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
		Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	
		Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.	
REFERENCE		1 (bases 1 to 1346)	
AUTHORS		Yamada,K., Iju,S.X., Pham,P.K., Banb,J., Banno,F., Dale,J.M., Goldsmith,A.D., Jiang,P.X., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C., Toriumi,M., Yamamura,Y., Yu,G., Yu,S., Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neuman,G., Kawai,J., Kim,C., Koeseema,E., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Natuska,M., Nguyen,M., Palm,C.J., Sakurai,T., Setou,M., Seki,M., Shinn,P., Southern,K.A., Tracy,S.E., Shimozaki,K., Davis,R.W., Eckert,J.R. and Theologis,A.	
TITLE		Full Length cDNA of gene MSJL_25/Atg15850 (GI:11994357)	
JOURNAL		Unpublished	
REFERENCE		2 (bases 1 to 1346)	

ACCESSION AF332433
 VERSION AF332433.1
 KEYWORDS GI:12083273
 SOURCE FLI_CDNA.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (bases 1 to 918)
 AUTHORS Yamada, K., Liu, S. X., Sakano, H., Pham, P. K., Banh, J., Egu, P., Lee, J. M., Toriumi, M., Yu, G., Brooks, S., Chao, Q., Chen, H., Karlin-Neumann, G., Kim, C., Lam, B., Miranda, M., Nguyen, M., Palm, C. J., Shinn, P., Southwick, A., Davis, R. W., Ecker, J. R. and Theologis, A.
 TITLE Full length cDNA of gene T21E18.13 (GI:8810470)
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 918)
 AUTHORS Yamada, K., Liu, S. X., Sakano, H., Pham, P. K., Banh, J., Egu, P., Lee, J. M., Toriumi, M., Yu, G., Brooks, S., Chao, Q., Chen, H., Karlin-Neumann, G., Kim, C., Lam, B., Miranda, M., Nguyen, M., Palm, C. J., Shinn, P., Southwick, A., Davis, R. W., Ecker, J. R. and Theologis, A.
 TITLE Direct Submission
 JOURNAL Submitted (28-DEC-2000) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
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 BASE COUNT 224 a 192 c 233 g 269 t
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 Matches 510; Conservative 0; Mismatches 325; Indels 9; Gaps 2;

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 Qy 499 tgaagcaaccataagtaaccataccaccagtgctgatacagaagaagatgtacatgcca 558
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 Qy 559 ctaagagatttggtgtcacatgttggtgggtcttgacaaagatttaattgctgaa 618
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 Db 470 A--GTGTGAGAGAGACAAATGTGGAGACTTAAAGACGAGTGTACTATAAATTC 526
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 Db 647 GCCTATTAACCTCTTGGCATGTTGGGAGCCGAACTTGAAGACTAATGACACT 706
 Qy 859 cgaccacataatgt 918
 Db 707 CCGTAACTGTTGGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 766
 Qy 919 acgattcgaacatacagctcgacacggtcgaagatgtgtgtgtgtgtgtgtgtgtgt 978
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 Db 827 AATATGTCGCTTTCGAGATATGCTTGGCTACTGATGATGATGATGATGATGATGATG 886
 Qy 1039 ctca 1042
 Db 887 GTCA 890
 RESULT 4
 D88536 1178 bp mRNA linear PLN 07-FEB-1999
 LOCUS Arabidopsis thaliana mRNA for delta 9 desaturase, complete cds.
 DEFINITION D88536.1 GI:2970033
 ACCESSION D88536.1
 KEYWORDS ADS1; delta 9 desaturase.
 SOURCE Arabidopsis thaliana
 ORGANISM Arabidopsis thaliana
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 REFERENCE 1 (bases 1 to 1178)
 AUTHORS Tasaka, Y.
 TITLE Direct Submission
 JOURNAL Submitted (24-OCT-1996) Yasushi Tasaka, National Institute for Basic Biology, Department of Regulation Biology; 38 Nishigonaka, Myodaijicho, Okazaki, Aichi 444, Japan (E-mail:tasakay@nibb.ac.jp, Tel:+81-564-55-7602, Fax:+81-564-54-4866)
 REFERENCE 2 (sites)
 AUTHORS Fukuchi-Mizutani, M., Tasaka, Y., Tanaka, Y., Ashikari, T., Kusumi, T. and Murata, N.
 TITLE Characterization of delta 9 acyl-1-lipid desaturase homologues from Arabidopsis thaliana
 JOURNAL Plant Cell Physiol. 39 (2), 247-253 (1998)
 MEDLINE 98220322
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Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1156)
REFERENCE  1
  AUTHORS  Tasaka, Y.
  TITLE    Direct Submission
  JOURNAL  Submitted (24-Oct-1996) Yasushi Tasaka, National Institute for
    Basic Biology, Department of Regulation Biology, 38 Nishiyonaka,
    Myodaiji-cho, Okazaki, Aichi 444, Japan (E-mail:tasakay@nibb.ac.jp,
    Tel:+81-564-55-7602, Fax:+81-564-54-4866)
  2 (sites)
REFERENCE  2
  AUTHORS  Fukuchi-Mizutani, M., Tasaka, Y., Tanaka, Y., Ashikari, T., Kusumi, T.
    and Murata, N.
  TITLE    Characterization of delta 9 acyl-11lipid desaturase homologues from
    Arabidopsis thaliana
  JOURNAL  Plant Cell Physiol. 39 (2), 247-253 (1998)
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ACCESSION	AY045918			
VERSION	AY045918.1	GI:15028190		
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SOURCE	thale cress.			
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AUTHORS	Yamada,K., Liu,S.X., Pham,P.K., Banh,J., Dale,J.M., Goldsmith,A.D., Jiang,P.X., Lee,J.M., Onodera,C.S., Quech,H.L., Tang,C., Toriumi,M., Yamamura,Y., Yu,G., Yu,S., Bowser,L., Carninci,P., Chen,H., Cheuk,R., Kawashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Koesema,E., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shim,P., Southwick,A., Tracy,S.E., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.			

TITLE Full length cDNA of gene T28P16.15/At2g31360 (GI:458964)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1253)
AUTHORS Yamada,K., Liu,S.X., Pham,P.K., Banh,J., Dale,J.M., Goldsmith,A.D., Jiang,P.X., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Yamamura,Y., Yu,G., Yu,S., Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamlya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Koesema,E., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinozaki,K., Shinozaki,T., Tracy,S.E., Hayashizaki,Y. and Davis,R.W., Ecker,J.R. and Theologis,A.
TITLE Submitted (09-Jun-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
JOURNAL RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-length cDNA') : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamlya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
COMMENT The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada,K., Liu,S.X., Pham,P.K., Banh,J., Dale,J.M., Goldsmith,A.D., Jiang,P.X., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Yamamura,Y., Yu,G., Yu,S., Bowser,L., Chen,H., Cheuk,R., Karlin-Neumann,G., Kim,C., Koesema,E., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinozaki,K., Shinozaki,T., Tracy,S.E., Davis,R.W., Ecker,J.R. and Theologis,A.
FEATURES

source	Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as PIs.
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TITLE	JOURNAL	REFERENCE	AUTHORS
TITLE	Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.	Full Length cDNA of gene T2IE18.17 (GI:8810474)	
JOURNAL	Unpublished	2 (bases 1 to 900)	
REFERENCE	Yamada, K., Liu, S.X., Sakano, H., Pham, P. K., Banh, J., Etgu, P., Lee, J.M., Toriumi, M., Yu, G., Brooks, S., Cho, O., Chen, H., Kallin-Neumann, G., Kim, C., Lam, B., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.	Direct Submission	
TITLE	Submitted (28-DEC-2000) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA		
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 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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 Rosidae; eurosids I; Rosales; Rosaceae; Rosoidae; Rosa.
 1 (bases 1 to 1153)
 Nishida,I.
 DIRECT SUBMISSION
 Submitted (16-FEB-1995) Ikuro Nishida, National Institute for Basic
 Biology, Cellular Regulation, 38 Nishigonaka, Myodaiji-cho,
 Okazaki, Aichi 444, Japan (E-mail:nishida@nib.ac.jp,
 Tel:0564-55-7602, Fax:0564-54-4866)
 2 (sites)
 REFERENCES
 AUTHORs Fukuchi-Mizutani,M., Savin,K., Cornish,E., Tanaka,Y., Ashikari,T.,
 Kusumi,T. and Murata,N.
 TITLE Senescence-induced expression of a homologue of delta 9 desaturase
 in rose petals
 JOURNAL Plant Mol. Biol. 29 (4), 627-635 (1995)
 MEDLINE 96128006
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 Db 172 ATCATAATATTTGGTGTGTC-----GGGTATGGGTGTAATATCTTACCATCGGAACCT 225
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RESULT 9
LOCUS D49385 1126 bp mRNA linear PLN 05-NOV-1997
DEFINITION Rose hybrida mRNA for delta-9 desaturase homologue, RP46.
ACCESSION D49385
VERSION D49385.1 GI:2580428
KEYWORDS Delta-9 desaturase.
SOURCE Rosa hybrida (strain:Kardinal) Senescence Petal cDNA to mRNA,
clone_11b:Lambda ZAPII clone:RP46.
ORGANISM Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.
REFERENCE 1 (bases 1 to 1126)
AUTHORS Nishida,I.
TITLE Direct Submission
JOURNAL Submitted (16-FEB-1995) Ikuo Nishida, National Institute for Basic
Biology, Cellular Regulation; 38 Nishigonaka, Myodaiji-cho,
Okazaki, Aichi 444, Japan (E-mail:nishidaenibb.ac.jp,
Tel:0564-55-7602, Fax:0564-54-4866)
2 (bases 1 to 1126)
REFERENCE Fukuchi-Mizutani,M., Savin,K., Cornish,E., Tanaka,Y., Ashikari,T.,
AUTHORS Kusumi,T. and Murata,N.
TITLE Senescence-induced expression of a homologue of delta 9 desaturase
JOURNAL In rose petals
MEDLINE Plant Mol. Biol. 29 (4), 627-635 (1995)
FEATURES
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LHNTYFLHSLVLLAGLVAGGLPVIWGMGVRYVVISQVFSSISICHTGKQIMDTG
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BASE COUNT 309 a 208 c 253 g 356 t
ORIGIN
Query Match 19.2%; Score 260; DB 8; Length 1126;
Best Local Similarity 59.0%; Pred. No. 3.5e-60;
Matches 487; Conservative 0; Mismatches 330; Indels 9; Gaps 2;

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OY 467 tctcgctctcagaggagatcccatggaatggtgagacacacataggtaccataccagct 526
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OY 527 cgtcgatcacagaagaatgtctcatagtcacacccaagaatttggtctgcacatcg 586
DB 350 TACGAAAAATTGAGACACCTCATACCCCATNAGGATTTGGTTTGTGCTCTGAA 409
OY 587 ttggtctctgacaaagattatctgcgcgaacacgctggtgcga--gaaacaaatc 643
DB 410 TTGGCTATTGATATATCATCTCGTTTGGAACTATACGAGACACTGATGAAGAAGCT 469
OY 644 gaatgattgaaagaacaaagcctctacagattctccgaaacatatatgtaccatca 703
DB 470 GCGAGATTGGAAATGCCAATATACATATAGTTTCTTATATACCTTCTCATTC 529
OY 704 attgacctaatagctacttacttactacgtcgagagggttccatactgctgggaat 763
DB 530 AGTCTCTTTCGAGTTCGACTCTATGTGCCGAGGATTTACCTTTGTGATTTGGGAAAT 589
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DB 590 GGGGTAAAGGTGAGTACATTTCCAAAGTTACTTTTCAATTAATTTATTTGCCACAC 649
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DB 650 TTGGGAAACAAATATGGATGCTGATCGTCAAAAACAACTGTTGTTGAATT 709
OY 884 gtgtcgcttggaagagcgtgcataacacacacacacacacacacacacacacacacacac 943
DB 710 GCTGGCATTCGAGACAGTTCGACAAATATACACCATGCTTTTGAATGATGATCGACCA 769
OY 944 cggcctagaatgctgcagatcgatgtactgtgtaacgttaccgaacctcaagcat 1003
DB 770 GGGCTTAGAACGTGGCAAAATTTGATACATGTTGATATGTGATTAAGTTTTCACAGTTGT 829
OY 1004 tggattggtctccaatgtgaagctaccacactggaagctcgaagaaga 1049
DB 830 GGGTTTGGCCACACGTAACCGCAACCGAATTCAGAAAGAA 875

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RESULT 10
LOCUS S80863 1126 bp mRNA linear PLN 27-MAR-1997
DEFINITION senescence-inducible gene [Rosa hybrida-roses, cv. Kardinal, day-4
post-harvest flowers, petals, mRNA Partial, 1126 nt].
ACCESSION S80863
VERSION S80863.1 GI:1911476
KEYWORDS
SOURCE Rosa hybrida cultivar petals cv. Kardinal day-4 post-harvest
flowers.
ORGANISM Rosa hybrida cultivar
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.
REFERENCE 1 (bases 1 to 1126)
AUTHORS Fukuchi-Mizutani,M., Savin,K., Cornish,E., Tanaka,Y., Ashikari,T.,
Kusumi,T. and Murata,N.
TITLE Senescence-induced expression of a homologue of delta 9 desaturase
JOURNAL In rose petals
MEDLINE Plant Mol. Biol. 29 (4), 627-635 (1995)
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gidsbp 175357] from the original journal article.
This sequence comes from Fig. 2.
FEATURES
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/organism="Rosa hybrida cultivar"
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/partial
/gene="senescence-inducible gene"
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CDS

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OY	467	tcctgccttcagaagagatcccaatggaaatgggttgagacaacatagatagatccatccaaagt	526
Db	267	tttgctaccttagaggtatctccacttggaatgggtgagacaccatagatattccacocattcatt	326
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OY	644	gaatcattctgagaagaacagctctctacagattccctccagaaaacttatatgtagacatca	703
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OY	704	attggtctaaatagctctacttacttactacgtcgagagggttccatcatcattgtctgggaat	763
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OY	764	gggtttatgatttgggttattatglttccatctcacttctgctatcgaactcaagttgtgcataa	823
Db	567	gggtgttaagggtgtgagtcattttcacaagcttactttttcaataaattttattttggccacac	626
OY	824	atggggcggaagggccatggaatcagatcgtgagatttatacgacaacaaatcgtttgtgcatt	883
Db	627	ttggggaaaacaaatattggcattctggtgattgcgtgcataaaaaaacattggttttggaatt	686
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Db	747	ggccttaaacacgcgtgcacaaattgattactagttggatgtgatttaagttttttccaagttgt	806
OY	1004	tggattgctacccaatgctgaagctcacaacatgaagctcagaagcaaa	1049
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DEFINITION		Arabidopsis thaliana putative delta 9 desaturase protein (T2D3.6)	
ACCESSION		AF332427	
VERSION		AF332427.1	
KEYWORDS		FLI CDNA.	
SOURCE		thale cress.	
ORGANISM		Arabidopsis thaliana	
REFERENCE		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
AUTHORS		Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	
		Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	
		1 (bases 1 to 900)	
		Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Etgu,P.,	
		Lee,J.M., Tortumt,M., Yu,G., Brooks,S., Chao,Q., Chen,H.,	
		Katlin-Neumann,C., Kim,C., Lam,B., Miranda,M., Nguyen,M.,	
		Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and	
		Theologis,A.	
TITLE		Full length cDNA of gene T2D3.6 (GI:89237673)	
JOURNAL		Unpublished	
REFERENCE		2 (bases 1 to 900)	
AUTHORS		Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Etgu,P.,	
		Lee,J.M., Tortumt,M., Yu,G., Brooks,S., Chao,Q., Chen,H.,	
		Katlin-Neumann,G., Kim,C., Lam,B., Miranda,M., Nguyen,M.,	
		Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and	
		Theologis,A.	

TITLE		Direct Submission	
JOURNAL		Submitted (28-DEC-2000) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA	
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Oy	375 ctgtgatacacttctgtcttccatcatagtgctcttactcatlbgcggtltcaagcttccaa	434	
Dd	208 CTCACGATCACATTCCTCATACCATATAGGAACCTTGGCTCACCGGACCTTTAAAGCTTCGGA	267	
Oy	435 ttgtgttgatctactcttctgacctcgtgtgctctccgcctcttcagggagatcccatgaa	494	
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Dd	348 TGGGTGACATATACATAGGCTTCATCACCAGATTCACAGATTTCGACCGTACCCACATAGC	387	
Oy	555 ccaactcaagcagatttctgtctcgttcaacatlggttgggtctcttgcaaaagattatctg	614	
Dd	388 CCTATCGAAGGATTTTGGTTGCTATGCTATGTGGATGATATGAGACATCGTTATATCAAA	447	
Oy	615 gaaaaacgtgtgtgcgcgaagaacaacatgtgaaatgttgaagaacaacgcttccacaga	674	
Dd	448 TATATGTGTGGAG---GACGTAAACAAGCTGATGAGACTTGAACACAAATGGTTTATATGG	504	
Oy	675 ttctctcsgaaaactatatactgatacacaatctgtgctctaaatagctcacttaactaag	734	
Dd	505 TTTTACGAAATGACATATGGTTTCCACGCTCTTAAAGTTTGGACGCTGCTCATATCTCAT	564	
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Dd	565 GGTGGTTTACCTTACATACATGCGCGCGGGCGGCGTGGAGAGTGATTTGGTACCACTGG	624	
Oy	795 acttcgcatacactcagtttctgataaataagggtgcggaagcgcatggaaatactggagat	854	
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QY 975 ttgtaagttatcagagctacaaagctatttgattgtgtcaccagtgtgaagctaccact 1034
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DB 865 GAATTCAGAAACAGAACT 884

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LOCUS 146889 819 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 2 from patent US 5639645.
ACCESSION 146889
VERSION 146889.1 GI:2470854
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 819)
AUTHORS Murata,N.
TITLRE Recombinant DELTA9 desaturase and a gene encoding the same
JOURNAL Patent: US 5639645-A 2 17-JUN-1997;
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BASE COUNT 182 a 181 c 190 g 266 t
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Query Match 14.0%; Score 189.4; DB 6; Length 819;
 Best Local Similarity 55.2%; Pred. No. 7,6e-41;
 Matches 417; Conservative 0; Mismatches 326; Indels 12; Gaps 2;

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DB 784 GCAACTAATGTCAACTAGACAGACAAAGAAGCAAGTA 818

RESULT 14
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AC E09606;
SV E09606.1
DX 08-OCT-1997 (Rel. 52, Created)
DT 02-SEP-2000 (Rel. 65, Last updated, Version 2)
XX gDNA encoding delta9 desaturase.
KW JP 1995170985-A/1.
OS unidentified.
OC unclassified.
XX [1]
RP 1-819
RA Murata N.;
RT *GENE CODING DELTA9 UNSATURATION ENZYME OF ANABAENA VARIABILIS*;
RL Patent number JP1995170985-A/1, 11-JUL-1995.
RL MITSUBISHI CORP, MITSUBISHI CHEM CORP, TOHOKU ELECTRIC POWER CO INC.
XX
OS Anabaena variabilis
CC PN JP 1995170985-A/1
CC PD 11-JUL-1995
CC CC 22-SEP-1993 JP 1993236719
CC PI MURATA NORIO
CC PC C12N15/09,C12N1/13,C12N1/21,(C12N1/13,C12N1:89),(C12N1/21,
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CC CC topology: Linear;
CC CC hypothetical: No;
CC CC anti-sense: No;
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Db 484 CTGGGGTGTGTGCTGTATATCTAGSGGGGTGCTTTGTGTGCTGSGGAGTTTCTTT 543
Oy 771 agattgggtttatgttccattccacttccgtatcaactcagttgtcataaatgggc 830
Db 544 CGCATCGTTTGGGTTTACCACTGTAAGTGTGTAACAGCGCTACCCATAGTTTGGC 603
Oy 831 ggaaggccaatggaatactgagattatcgaaccacaataatgtttgtcattgtgtgcg 890
Db 604 TACCGACCTATGATGCTGTGTGACAGATCCACTAATCTTTGGTGGGTAGCTGTCTAGTG 663
Oy 891 ttggagagggtcgtgcatacaacaacacgaatcgaacaaatcagctcgaacagggcta 950
Db 664 TTTGGTGAAGTTGGCAACAACACACGCTTTCATATATTCAGCTCGTCACGGGTTG 723
Oy 951 gaatggtgcagatcgaatgttacttggtaagttatcaagaactcaagaactatlgatg 1010
Db 724 GAATGGTGGGAAGTTGATCTGACTTGGATGACAGTGCATTTGCTGCAATACTCGGTTTA 783
Oy 1011 gctaccaatgtgaagcttaccactgaagctcagaa 1045
Db 784 GCAACTAATGTCAAACTAGCAGACAAAAGCAGTA 818

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Search completed: September 13, 2002, 08:45:45
 Job time: 7370 sec

XX Cahoone EB, Hiltz WD, Kinney AJ, Vollmer SU;
PI
XX
XX WPI; 1999-591101/50.
DR
DR P-PSDB; AAY39361.
XX
XX
PI Nucleic acid fragments useful in the production of industrial agents
for eg. lubricants or cosmetics -
XX
PS Claim 2, Page 46; 54pp; English.

This sequence is the *Limnanthes douglasii* delta-5 acyl-CoA desaturase cDNA. The delta-5 desaturase introduces a double bond at the delta 5 position of a C20 fatty acid. Delta-5 desaturase is an enzyme which is able to further desaturate mono-unsaturated fatty acids to make poly-unsaturated fatty acids. Fatty acids are used in plant membranes and in neutral lipids that are formed for the storage of energy in developing seed tissue. This nucleotide sequence can be linked to regulatory sequences and used to transform host cells. The invention also reveals a fatty acyl-CoA elongase cDNA sequence (AAZ2816), this enzyme prefers palmitoyl-CoA (16:0-CoA) as its substrate instead of oleoyl-CoA (18:1-CoA) the usual substrate for the known plant fatty acid elongase. The nucleic acid sequences of the delta-5 desaturase and the acyl-CoA elongase can be used in genetic engineering to manipulate fatty acid biosynthetic pathways, allowing changes to be made in the fatty acid composition of plants and/or oils and to introduce new pathways in to oil seeds in order to produce new biopolymers from acyl-CoA. The oils and fatty acids produced by the genetically engineered plants have potential for use as industrial agents including lubricants, greases, plastics, inks, cosmetics and surfactants. Polysatolides derived from the 20:1 delta-5 fatty acids of *Limnanthes* biodegrade slower than those derived from soybean oils or oleic oils, and thus will produce industrial products with a longer shelf life.

50 Sequence 1355 BP; 355 A; 283 C; 299 G; 418 T; 0 other;

Query Match	100.0%	Score 1355;	DB 20;	Length 1355;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1355; Conservative	0;	Mismatches	0;	Gaps 0;

[illegible]

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QY	601	aagatttatctcgtcgaaaaacgvtgvtggtccgaagaacaaagtgaatgttgaagaac	660
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Db	661	aagcctttacaagatctcctccagaanaacttatatgataccaataatgggtcctaaggtc	720
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KW	protein identification; signal transduction pathway;
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AC	AAC39176;
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DT	17-Oct-2000 (first entry)

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KW	Hybridisation assay; genetic mapping; gene expression control;	
KW	protein identification; signal transduction pathway;	
KW	metabolic pathway; promoter; termination sequence; ss.	
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OS	Arabidopsis thaliana.	
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DB 488 ctctcgggattactctgtcttccaagaagtaacttctcataaagccttcaagctact 547
OY 432 aagtggttgaattactcttctgctactgttgcctctctcgccttcaaggagatcccaag 491
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DB 548 aaatggcttgagtaacttctgtcttactatgttggagctcaagccttcaaggaaacccaatt 607
OY 492 gaattgggtggaacacatgtaacatcacccagctcgcgtccatcacacaagaagatgttcat 551
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DB 608 gatitgggtgagtaacataatgtaacatacctcaagtttggatcagacagaaacctcat 667
OY 552 agtccaactcaaggatttggctcgtcgaacttgggttcttgacaaagaattatc 611
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DB 668 agccaacttgaatgttcttggctcagtcacatgaatttgaatttggatccacaactac 727
OY 612 gtccgaaaacgtgtgtgcggaagaacaaatgtaatttgaagaagaacaccttctac 671
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DB 965 gatttctcgaagaacactgtgtgtgtgtagcagctcgtacatcgtgggaagatggtcacac 1024
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DB 1025 aatcacacagcttcttggatctcagctcagcagcagcttagaatgtgtgcaacttgaatg 1084
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RESULT 4
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AAC38595;

17-OCT-2000 (first entry)

Arabidopsis thaliana DNA fragment SEQ ID NO: 21544.

Hybridisation assay; genetic mapping; gene expression control;
protein identification; signal transduction pathway;
metabolic pathway; promoter; termination sequence; ss.

Arabidopsis thaliana.

EP1033405-A2.

06-SEP-2000.

25-FEB-2000; 2000EP-0301439.

25-FEB-1999; 99US-0121825.

05-MAR-1999; 99US-0123180.

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PR 31-AUG-1999; 99US-0151438.
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PR 26-OCT-1999; 99US-0161361.

PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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Best Local Similarity	62.2%	Pred. NO. 2.9e-77;		
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OY	195	tcaaaatcgtgtgttgsgaggaagaaatccaaaggttcctgctgcgcgsgaaagaaacccctgt	254
Db	246	tcgaaagctctgtgtgtgtgaagaacgaagagtgcaattcttgysgaaagagatgtgagactctgtg	305
OY	255	gatatccaagaacgcgcgcacacttactactgtgtctccatgctctcttcgaacgagatctggcccttt	314
Db	306	gagctgagcgaagttagtaaatatctgcctgggaaccatcttgtagccctctgtctccatctt	365
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Db	366	tactccagtttggagsgctcttttggg----tttcccttgcctgtgttttc--atcaatgga	419
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Db	420	atctgcgaattacactgtgtctctcatatagaaacacttctccacogaaggttttgatctgcgcga	479
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OY	735	ggagsggttccatatacatctgtctcgsggaatvggttttagatvtggtttatgttccattcc	794
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OY	795	acttgcctatcaactaagtcttggttcaataatgtggsggaagccatcaggaatacttggagt	854
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OY	855	ttaatcgacccaacataatgtttgttgcattgtgtgtgtgttgagagaggtcgtgcgataacaac	914
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OY	915	caccacagcatctgacaacatcaagctcgacacgcggtcagatagatvtgtgcagatcgatctact	974
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Query Match      21.0%; Score 284.4; DB 21; Length 1105;
Best Local Similarity 60.3%; Pred. NO. 9.8e-72;
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DB 308 tcaagatcttctctgctattgtcgccctcttgcattcaagggagatccgaatgattgg 367
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DB 488 a---gtgtgaagaagagacaatgttggaagacttaagaagcagtggtactataatcc 544
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KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
PN EP1033405-A2.
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XX 25-FEB-2000; 2000EP-0301439.
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 DB 112 agattagattatggaattctcagctcttcaacgttcaatctctctgctcctcttgct 171
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 DB 172 ccgttattatcacttgctgcgcctcttggtttacgttttgctt-----ttacacatc 225
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DB 226 ggtgtcttgatcacccgtctctatcatcgcgaacttggtctccgcgagtttcaagtc 285
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 KW Hybridisation assay; genetic mapping; gene expression control;
 KW protein identification; signal transduction pathway;
 KW metabolic pathway; promoter; termination sequence; ss.
 OS Arabidopsis thaliana.
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 PD 06-SEP-2000.
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DB 75 gcggtcgctgggggaaagagcattattcttcggaatgagccggatcgattagcg 134
    || || || || || || || || || || || || || || || || || || || || ||
OY 264 aacgcgcgtcaattactgctgctcgtcttcgacgagtcgagcccttatttcagc 323
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DB 135 agagcttcgagctgctggggcgctgacatctgctgctgctgcttcgaataaa 194
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DB 195 tgggaagctcccgctcgctgctgctgctgctgctgctgctgctgctgctgctgct 248
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DB 546 aacacaaatgtgctccacatcttaacatcttgcagccctgctctatcttaagtggtgctcta 605
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OY 1044 aagcaaaa 1051
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DB 906 aagcgaaa 913

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RESULT 10

AAC39817 standard; DNA; 1150 BP.

AAC39817;

17-OCT-2000 (first entry)

Arabidopsis thaliana DNA fragment SEQ ID NO: 26011.

Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

KM metabolic pathway; promoter; termination sequence; ss.

Arabidopsis thaliana.

EP1033405-A2.

06-SEP-2000.

25-FEB-2000; 2000EP-0301439.

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05-MAR-1999; 99US-0123180.

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23-MAR-1999; 99US-0125788.

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OY 315 taattcagctggagatgcttctgagctcttcttctgcttctgcttctgcaaggggtt 374
DB 196 aactacaaatggagacattcggctgcttctgcttctgcttctgcttctgcttctgctt 249
OY 375 ctgtgtatcaactctgtcttcaatagtgcttcttcaatggcggttcaagcttcaag 434
DB 250 ctgcagcatcatcttcatlaccatagaaacttgctcacggagcttcaagcttcaagaa 309
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DB 967 aatttcaact 977

RESULT 11

AAC39174
ID AAC39174 standard; DNA; 1114 BP.
XX
AC AAC39174;
XX
XX 17-OCT-2000 (first entry)
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 23649.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
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XX 25-FEB-1999; 99US-0121825.
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PR 09-MAR-1999; 99US-0123548.
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[illegible]

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XX EP644263-A.
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XX
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PF
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XX 22-SEP-1993; 93JP-0236720.
PR
XX
XX (MURA/) MURATA N.
PA (MITU ) MITSUBISHI CHEM IND LTD.
PA (MITS ) MITSUBISHI CORP.
PA (TOEL ) TOHOKU ELECTRIC POWER CO.
PI
PI Murata N:
PI
PI WPI: 1995-116988/16.
DR P-PSDB: AAR70259.
XX
XX New isolated gene encoding delta 9 desaturase of cyanobacteria -
PT useful for transforming plants, animals or microorganisms to
PT improve low temp. tolerance
XX
XX Claim 3: Page 8-10; 14pp; English.
XX
XX A genomic DNA library of Synechocystis sp. PCC6803 was screened
XX using the coding sequence of Anabaena variabilis delta-9-desaturase
XX (desc(A)) as probe. Subsequent plaque hybridization using a 0.75 kb
XX fragment of the Anabaena desc(A) gene was used to identify the
XX desc protein coding region given in AM083640. Lipids in E. coli
XX transformants expressing the Synechocystis desc gene had modified
XX fatty acid composition.
SQ Sequence 957 BP; 216 A; 216 C; 200 G; 325 T; 0 other;

Query Match 11.7%; Score 158.8; DB 16; Length 957;
Best Local Similarly 52.5%; Pred. No. 1,7e-35;
Matches 402; Conservative 0; Mismatches 352; Indels 12; Gaps 2;

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OY 346 ttatctctgctgcttgcgaagcgctgcttctggtacacttctgcttccatgagctc 405
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XX Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway;
XX metabolic pathway; promoter; termination sequence; ss.
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XX Arabidopsis thaliana.
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XX EPI033405-A2.
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XX 25-FEB-2000; 2000EP-0301439.
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PR 29-OCT-1999: 99US-0162142.

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Matches 205; Conservative 0; Mismatches 162; Indels 0; Gaps 0;

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Search completed: September 13, 2002, 08:50:53
Job time: 4543 sec

GenCore version 4.5
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OM nucleotide - nucleotide search, using sw model

Run on: September 13, 2002, 06:44:30 ; Search time 52.22 Seconds

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Title: US-09-664-840-1

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Searched: 363533 seqs, 122816752 residues

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Minimum DB seq length: 0
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	102.2	7.5	837	3	US-08-663-082-3
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5	48.8	3.6	546	2	US-08-558-823-9
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C 38	33.8	2.5	2443	5	PCT-US96-07528-1	Sequence 1, Appl1
C 39	33.8	2.5	2561	4	US-09-146-221-7	Sequence 7, Appl1
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C 45	33.6	2.5	3714	4	US-09-087-465-9	Sequence 9, Appl1

ALIGNMENTS

RESULT 1
US-08-309-182B-2
Sequence 2, Application US/08309182B
Patent No. 5639645
GENERAL INFORMATION:
APPLICANT: No. 5639645io MURATA
TITLE OF INVENTION: A RECOMBINANT 9 DESATURASE AND A GENE
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
City: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
OPERATING SYSTEM: IBM compatible
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/309,182B
FILING DATE: September 20, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 819 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORGANISM: Anabaena variabilis
FEATURE:
NAME/KEY: CDS
LOCATION: 1..816
IDENTIFICATION METHOD: P
US-08-309-182B-2

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RESULT 3

US-08-663-082-3
 ; Sequence 3, Application US/08663082
 ; Patent No. 6043411

GENERAL INFORMATION:

APPLICANT: NISHIZAWA, Osamu
 APPLICANT: TOGURI, Toshihiro
 TITLE OF INVENTION: GENE FOR FATTY ACID DESATURASE, VECTOR
 TITLE OF INVENTION: CONTAINING SAID GENE, PLANT TRANSFORMED WITH SAID GENE,
 AND PROCESS FOR CREATING SAID PLANT
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 City: Washington
 STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/663,082

FILING DATE: 25-JUN-1996

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/JP94/02288

FILING DATE: 28-DEC-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 93/352858

FILING DATE: 28-DEC-1993

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 81356/107

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 837 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

ORIGINAL SOURCE:

ORGANISM: Anacystis nidulans

STRAIN: R2-SPC

US-08-663-082-3

Query Match 7.5%; Score 102.2; DB 3; length 837;
 Best Local Similarity 49.2%; Pred. No. 1.2e-21;
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RESULT 4

US-08-742-273-1
 ; Sequence 1, Application US/08742273
 ; Patent No. 5777201

GENERAL INFORMATION:

APPLICANT: Mehra-Palta, A.

TITLE OF INVENTION: Modification of Vegetable Oils using

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lubrizol Corporation

STREET: 29400 Lakeland Boulevard

CITY: Wickliffe

STATE: OH

COUNTRY: USA

ZIP: 44092

COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,273
FILING DATE: 31-OCT-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/222,553
FILING DATE:
APPLICATION NUMBER: US 07/850,714
FILING DATE: 13-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Cairns, James A.
REGISTRATION NUMBER: 32557
REFERENCE/DOCKET NUMBER: 2613
TELECOMMUNICATION INFORMATION:
TELEPHONE: 216-943-4200
TELEFAX: 216-943-0748
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1782 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Saccharomyces cerevisiae
FEATURE:
NAME/KEY: CDS
LOCATION: 106..1635
US-08-742-273-1

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Query Match          3.6%; Score 49; DB 1; Length 1782;
Best Local Similarity 44.6%; Pred. No. 3.8e-05;
Matches 295; Conservative 0; Mismatches 350; Indels 16; Gaps 2;

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340 tctctttaaactgcttggttccgaagcggtctcttgtagtaacttggcttcacata 399
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Qy 400 ggtgttctaactgaagcggttctcaagcttcaagttggttgtagtaacttggcttact 459
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Db 1068 caactcagtttagctgccttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgt 1127
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Qy 986 c 986
Db 1188 c 1188

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RESULT 5
US-08-558-823-9
Sequence 9, Application US/08558823
Patent No. 5876994
GENERAL INFORMATION:
APPLICANT: Knipple, Douglas C.
APPLICANT: Roelofs, Wendell L.
APPLICANT: Miller, Stuart J.
TITLE OF INVENTION: PHEROMONE DESATURASES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/558,823
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Rogalsky Esq., Peter
REGISTRATION NUMBER: 38,601
REFERENCE/DOCKET NUMBER: 19603/400
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1634
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 546 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-558-823-9

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Query Match          3.6%; Score 48.8; DB 2; Length 546;
Best Local Similarity 47.3%; Pred. No. 2.2e-05;
Matches 227; Conservative 3; Mismatches 225; Indels 25; Gaps 2;

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464 ctctcgtctcttcgaaggagatcccaatggaattggttggaacacatagttaccatcacca 523
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Qy 534 gttcgtcgcatacagaagaagatgttcatagtcacaactcaagatttggctctgacat 583
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Db 129 atacagcatatctgattgattcccccacaaatgcctcaagagggttcttactgcgaatg 188
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Qy 584 tgggttgggttcttgcaagaatttatctgcgaagaacggtggtgcgaagaagaacatgt 643
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Db 189 TGGCTGGCTATTAGTAAAAAACATCCCGAGCTCCTGAATATGCAAAACTATAGACAT 248
QY 644 gaatgatttgaagaagaagccttctacagattccctcagaanaactatatacaccatca 703
Db 249 GTCGAGATGATACAAATATCTGTGTAAATTT--TCAGAAAAGATGACGAGTACCTTA 306
QY 704 attgagcttaagcttacttcttctacgctcgcgaggggttccatacattgtctgggaat 763
Db 307 ATTGGAACAGTTTGTGTGCTTCACAACTTTGATTCAGTCTGTGTGGGGGAATCG 366
QY 764 gggT-----ttagattggttattatgttccattccattcc 800
Db 367 TGGAAACAAGCTTGGACATAGCCTTATTTTCATATTTCAATCTTAAAGTACCTTTC 426
QY 801 gctacacactcaagtttgcataaataaggcggaagccatggaatctgagattatcg 860
Db 427 CTACTCAACAGTGTGCTGCAATATCTGGGGGAAATTAAGCTTATGATTAAGCATCTTGCC 486
QY 861 accacacataatgttgtgattgattgctgcttggagagggcgtgcaataacacacac 920
Db 487 GCTCAAAACCTGCTGTTTCTCTTCTAGCAAGTGGAGAGGCTTCCATTAATTCACATCAC 546

RESULT 6

US-08-558-823-8

Sequence 8, Application US/08558823

Patent No. 5876994

GENERAL INFORMATION:

APPLICANT: Knipfle, Douglas C.

APPLICANT: Roelofs, Wendell L.

APPLICANT: Miller, Stuart J.

TITLE OF INVENTION: PHEROMONE DESATURASES

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP

STREET: Clinton Square, P.O. Box 1051

CITY: Rochester

STATE: New York

COUNTRY: U.S.A.

ZIP: 14603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/558,823

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Rogalsky, Esq., Peter

REGISTRATION NUMBER: 38,601

REFERENCE/DOCKET NUMBER: 19603/400

TELEPHONE: (716) 263-1634

TELEFAX: (716) 263-1600

INFORMATION FOR SEQ. ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 1047 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-558-823-8

Query Match 3.6%; Score 48.6; DB 2; Length 1047;
Best Local Similarity 47.6%; Pred. No. 3.7e-05;
Matches 231; Conservative 0; Mismatches 229; Indels 25; Gaps 2;

QY 464 cttctcgccttcacggagagatccatcgatgtggagcaacataggtaccatca 523
Db 324 CTTCTTAGCTTTTCAAAACAGCGCTATTACCTGGCTAGAGAACATCGGCTCATCATCA 383

QY 524 gtctcgatatacagaagaagatgttcatagctccaaactcaaggatttggcttcgacat 583
Db 384 ATACAGGATACATGATCTGATCTATCCCAATATGCTCAAGAGGTTCTTACTGCAATGT 443
QY 584 tggttgggttccttgacaagaattatctcgtcgaanaacgttggccgaagaacaaatgt 643
Db 444 TGGCTGGCTATTAGTAAAAAACATCCCGAGCTCCTGAATATGCAAAACTATAGACAT 503
QY 644 gaatgatttgaagaagaagccttctacagattccctcagaanaactatatacaccatca 703
Db 504 GTCGAGATGATACAAATATCTGTGTAAATTT--TCAGAAAAGATGACGAGTACCTTA 561
QY 704 attgagcttaagcttacttcttctacgctcgcgaggggttccatacattgtctgggaat 763
Db 562 ATTGGAACAGTTTGTGTGCTTCACAACTTTGATTCAGTCTGTGTGGGGGAATCG 621
QY 764 gggT-----ttagattggttattatgttccattccattcc 800
Db 622 TGGAAACAAGCTTGGACATAGCCTTATTTTCATATTTCAATCTTAAAGTACCTTTC 681
QY 801 gctacacactcaagtttgcataaataaggcggaagccatggaatctgagattatcg 860
Db 682 CTAGTCAACAGTGTGCTGCAATATCTGGGGGAAATTAAGCTTATGATTAAGCATCTTGCC 741
QY 861 accacacataatgttgtgattgattgctgcttggagagggcgtgcaataacacacac 920
Db 742 GCTCAAAACCTGCTGTTTCTCTTCTAGCAAGTGGAGAGGCTTCCATTAATTCACATCAC 801
QY 921 gcat 925
Db 802 GTCCT 806

RESULT 7

US-08-663-082-1

Sequence 1, Application US/08663082

Patent No. 6043411

GENERAL INFORMATION:

APPLICANT: NISHIZAWA, Osamu

APPLICANT: TOGURI, Toshihiro

TITLE OF INVENTION: GENE FOR FATTY ACID DESATURASE, VECTOR

TITLE OF INVENTION: CONTAINING SAID GENE, PLANT TRANSFORMED WITH SAID GENE,

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/663,082

FILING DATE: 25-JUN-1996

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/JP94/02288

FILING DATE: 28-DEC-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 93/352858

FILING DATE: 28-DEC-1993

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 81356/107

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300


```

1 NAME: Warren M. Cheek, Jr.
2 REGISTRATION NUMBER: 33,367
3 REFERENCE/DOCKET NUMBER:
4 TELECOMMUNICATION INFORMATION:
5 TELEPHONE: 202-371-8850
6 TELEFAX: 202-371-8856
7
8 INFORMATION FOR SEQ ID NO: 7:
9
10 SEQUENCE CHARACTERISTICS:
11     LENGTH: 1355 base pairs
12     TYPE: nucleic acid
13     STRANDEDNESS: double
14     TOPOLOGY: linear
15
16 MOLECULE TYPE: cDNA to mRNA
17
18 HYPOTHETICAL:
19
20 ANTI-SENSE:
21
22 FRAGMENT TYPE:
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24 ORIGINAL SOURCE:
25     ORGANISM: Candida albicans
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27 STRAIN:
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29 INDIVIDUAL ISOLATE:
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31 DEVELOPMENTAL STAGE:
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33 HAPLOTYPE:
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35 TISSUE TYPE:
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37 CELL LINE:
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39 ORGANELLE:
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41 IMMEDIATE SOURCE:
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43 LIBRARY:
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45 CLONE:
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47 POSITION IN GENOME:
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49 CHROMOSOME/SEGMENT:
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51 MAP POSITION:
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57     NAME/KEY:
58     LOCATION: 165-1187
59     IDENTIFICATION METHOD:
60     OTHER INFORMATION: /note=
61     OTHER INFORMATION: "E CDS (secretary aspartic proteinase)"
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63     FEATURE:
64     NAME/KEY:
65     LOCATION: 1336-1355
66     IDENTIFICATION METHOD:
67     OTHER INFORMATION: /note= "E poly A site"
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69 PUBLICATION INFORMATION:
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71     AUTHORS:
72     TITLE:
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74 JOURNAL:
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76 VOLUME:
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78 ISSUE:
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80 PAGES:
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82 DATE:
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84 DOCUMENT NUMBER:
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86 FILING DATE:
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88 PUBLICATION DATE:
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90 RELEVANT RESIDUES IN SEQ ID NO:
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	Query Match	2.8%	Score 37.6;	DB 1,	length 1355;	
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OY	1292	actgatctgtgtgtgtcacgtttcgagaatatagatgtttcttcgttcacaaaaaa	1351			
Db	1286	AACCTTTTGGCTTCCTTCAGAAGTTTTTTTATTTGTGTTTTOTAAAAAAAAA	1345			
OY	1352	aaaa 1355				

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RESULT 15 -
 S-09-018-584A-13
 Sequence 13, Application US/09018584A
 Patent No. 6238863
 GENERAL INFORMATION:
 APPLICANT: Schumm, James W.
 APPLICANT: Bachert, Jeffrey W.
 TITLE OF INVENTION: MATERIALS AND METHODS FOR
 IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM

Fri Sep 13 15:31:12 2002

us-09-664-840-1.rni

Page 10

```

1 TITLE OF INVENTION: REPEAT DNA MARKERS
2 NUMBER OF SEQUENCES: 147
3 CORRESPONDENCE ADDRESS:
4 ADDRESSEE: Promega Corporation
5 STREET: 2800 Woods Hollow Road
6 City: Madison
7 STATE: Wisconsin
8 COUNTRY: U.S.A.
9 ZIP: 53711-5399
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
12 COMPUTER: IBM compatible PC
13 OPERATING SYSTEM: Windows 95
14 SOFTWARE: Word 97 (DOS text format)
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER: US/09/018,584A
17 FILING DATE: 04-Feb-1998
18 CLASSIFICATION:
19 ATTORNEY/AGENT INFORMATION:
20 NAME: Grady J. Prentchick
21 REGISTRATION NUMBER: 29,018
22 REFERENCE/DOCKET NUMBER: 16026.9180
23 TELECOMMUNICATION INFORMATION:
24 TELEPHONE: (608) 257-3501
25 TELEFAX: (608) 257-2275
26 INFORMATION FOR SEQ ID NO: 13:
27 SEQUENCE CHARACTERISTICS:
28 LENGTH: 372 bp
29 TYPE: Nucleic Acid
30 STRANDEDNESS: Double
31 TOPOLOGY: Circular
32 MOLECULE TYPE: Genomic DNA
33 HYPOTHETICAL: no
34 IMMEDIATE SOURCE:
35 LIBRARY: plasmid, pGem3Zf(+)
36 CLONE: G132
37 POSITION IN GENOME:
38 CHROMOSOME/SEGMENT: 4 qter
39 US-09-018-584A-13

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	Best Local Similarity	58.9%;	Pred. NO. 0.1;	Mismatches 44;	Indels 0; Gaps 0.
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Db	120	tctctctctcccttcctctctctctctctctctctctctctctctctcccttc	179		
Oy	70	tcatgaacaacaaacaccgaatgcagcttgctgattgtctt	116		
Dd	180	cctttccctttcccctttccctttccctttccctttccattttttt	226		

Search completed: September 13, 2002, 08:46:55
Job time: 7345 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 13, 2002, 06:38:55 ; Search time 1767.26 Seconds

(without alignments)
10348.434 Million cell updates/sec

Title: US-09-664-840-1

Perfect score: 1355

Sequence: 1 gcttgagactctctctctac.....ttgtgtcacaataaaaaa 1355

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

EST:*
1: em_earth:*
2: em_earth:*
3: em_earth:*
4: em_earth:*
5: em_earth:*
6: em_earth:*
7: em_earth:*
8: em_earth:*
9: gb_est1:*
10: gb_est2:*
11: gb_est3:*
12: gb_est4:*
13: gb_est5:*
14: em_gss_hum:*
15: em_gss_hum:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	259.2	19.1	590	10	BF053048 EST438278
2	203.6	15.0	503	10	BE802366 sr29b07 y
3	181.6	13.4	528	10	BE919440 EST423125
4	179.4	13.2	564	9	AV439619 AV439619
5	171.6	12.7	691	10	AV439619 AV439619
6	167.6	12.4	556	9	AV442617 AV442617
7	160.8	11.9	552	9	AV551184 AV551184
8	155.4	11.5	680	10	AV551184 AV551184
9	152.8	11.3	513	9	AV550066 AV550066
10	152.4	11.2	522	9	AV550066 AV550066
11	142.4	10.5	494	9	AV550066 AV550066
12	142.2	10.5	700	10	AV550066 AV550066
13	142	10.5	721	10	AV550066 AV550066
14	141.8	10.5	660	10	AV550066 AV550066
15	139.4	10.3	458	9	AV550066 AV550066
16	139.4	10.3	520	9	AV550066 AV550066
17	139	10.3	520	9	AV550066 AV550066

18	138	10.2	701	9	AI483228
19	129.6	9.6	598	9	AV539911
20	128.8	9.5	428	10	BI720501
21	126.2	9.3	313	9	AI782644
22	124.4	9.2	592	9	AV539024
23	123.2	9.1	492	9	AV544942
24	122.6	9.0	389	10	T46147
25	122	9.0	447	9	AI992605
26	121.6	9.0	281	9	AI782643
27	118.8	8.8	600	9	AV539795
28	117.6	8.7	600	9	AV538469
29	114.8	8.5	523	9	AV538985
30	114.8	8.5	536	9	AV542250
31	113.6	8.4	540	9	AA041026
32	113.4	8.4	395	10	T20690
33	111.6	8.2	602	9	AV538452
34	106.6	7.9	479	9	AV539783
35	97.6	7.2	341	10	Z30751
36	94.6	7.0	375	9	AV551324
37	93.2	6.9	784	12	BH578290
38	92.8	6.8	501	9	AV539361
39	92	6.8	615	9	AI483237
40	87.2	6.4	720	12	BH438059
41	86.8	6.4	522	10	N97264
42	86.4	6.4	406	9	AV539450
43	85.6	6.3	412	9	AV539469
44	81.2	6.0	663	10	BG129876
45	81	6.0	418	10	Z32595

ALIGNMENTS

RESULT 1
LOCUS BF053048
DEFINITION EST438278 potato leaves and petioles Solanum tuberosum cDNA clone
CSTB34E7 5' sequence, mRNA sequence.
ACCESSION BF053048.1 GI:10806944
VERSION
KEYWORDS
SOURCE
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 590)
AUTHORS van der Hoeven R.S., Bezzerides J., Holt I.E., Liang F., Cho J., Uiterback T., Hansen C.L., Doan B., Bougri O., Buell C.R., Ronning C.M., Fry W.E., Tanksley S.D. and Baker B.
Generation of ESTs from potato leaves and petioles
Unpublished (2000)
Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: Please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdna@resgen.com.
JOURNAL
COMMENT
TITLE
FEATURES
source
1..590
/organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="CSTB34E7"
/clone_1lb="potato leaves and petioles"
/tissue_type="leaves and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Tissue was supplied by Dr. Fry (Cornell University). leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in liquid nitrogen."

BASE COUNT

152 a 112 c 152 g 174 t

Db 427 TATATGACGAGGAGGATTCCTTCTTGTAGGGAATGGAGTGAGATTG 480

RESULT 3

BE919440

LOCUS EST423125 potato leaves and petioles Solanum tuberosum cDNA clone

DEFINITION EST423125 potato leaves and petioles Solanum tuberosum cDNA clone

ACCESSION BE919440

VERSION BE919440.1 GI:10445432

KEYWORDS EST.

SOURCE Solanum tuberosum

ORGANISM Solanum tuberosum

REFERENCE 1 (bases 1 to 528)

AUTHORS van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J.,

Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Romling

, C.M., Fry, W.E., Tanksley, S.D. and Baker, B.

Unpublished (2000)

CONTACT: Cathy Romling

The Institute for Genomic Research

For clone request: please contact Research Genetics, Labarles

Division tel 1-800-711-6195, email cdnaregen.com.

LOCATION/Qualifiers

1..528

/organism="Solanum tuberosum"

/cultivar="Kennebec"

/db_xref="taxon:4113"

/clone="EST423125"

/clone_lib="potato leaves and petioles"

/tissue_type="leaflets and petioles"

/dev_stage="8 weeks old plants"

/lab_host="SOLR"

/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:

XhoI; Tissue was supplied by Dr. Fry (Cornell University).

Leaflets and petioles were isolated from 8 week old

greenhouse grown plants. The plants were watered and

fertilized freely. The tissue was immediately frozen in

liquid nitrogen.

BASE COUNT 129 a 103 c 128 g 168 t

ORIGIN

Query Match 13.4%; Score 181.6; DB 10; Length 528;
Best Local Similarity 61.9%; Pred. No. 5.3e-31;
Matches 322; Conservative 0; Mismatches 194; Indels 4; Gaps 2;

Db 309 TGGGAAGCCCAACATGTGGGGGATTTGGAGACGAGTTTATATCATCTTCGTGA 368

RESULT 4

AV439619/c

LOCUS AV439619 564 bp mRNA linear EST 14-NOV-2000

DEFINITION AV439619 Arabidopsis thaliana above-ground organ two to six-week

old Arabidopsis thaliana cDNA clone ABD07f11.f 3', mRNA sequence.

ACCESSION AV439619

VERSION AV439619.1 GI:7609961

KEYWORDS EST.

SOURCE thale cress.

ORGANISM Arabidopsis thaliana

REFERENCE 1 (bases 1 to 564)

AUTHORS Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.

A large scale analysis of cDNA in Arabidopsis thaliana: Generation

of 12,028 non-redundant expressed sequence tags from normalized and

size-selected cDNA libraries

DNA Res. 7, 175-180 (2000)

CONTACT: Erika Asamizu

The First Laboratory for Plant Gene Research

Kazusa DNA Research Institute

Yama 1532-3, Misarazu, Chiba 292-0812, Japan

Email: asamizu@kazusa.or.jp. URL: http://www.kazusa.or.jp/en/plant/.

LOCATION/Qualifiers

1..564

/organism="Arabidopsis thaliana"

/strain="Columbia"

/db_xref="taxon:3702"

/clone="ABD07f11.f"

/clone_lib="Arabidopsis thaliana above-ground organ two to

six-week old"

/tissue_type="above-ground organs"

/dev_stage="two to six-week old"

/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:

XhoI"

BASE COUNT 168 a 136 c 104 g 156 t

ORIGIN

Query Match 13.2%; Score 179.4; DB 9; Length 564;
Best Local Similarity 64.6%; Pred. No. 1.7e-30;
Matches 267; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

Db 384 TTGTCTAGACACACTGCTGGTAGCAGCTCTAGCATTGGGGAGAGATGACACACAA 325
 Oy 914 coacacagcattcgacacatcagctcgacacgagctagaatgtgtgcagatcgatgttac 973
 Db 324 TCACCATGCTTTTGTAGTCTCAGTCGACGGCGCTTAGAAGTGTGGCAACTGTGATATGAC 265
 Oy 974 ttgtgaagttatcagactctacacagctatggattggctaccatgtgaagctacacaa 1033
 Db 264 TTGTGATGCTGTTAAGTCTTCAAGCCATCGTTTACCACTGATGTCAGACCTCCATC 205
 Oy 1034 tgaagctcagaacaaagctcaagaagagtgcttaaggagtttgaagca 1086
 Db 204 GGAAGCTGAGAACAAAGATGCGATTCACGCGACTGATCTTAAAGAAATGA 152
 RESULT 5
 BUI67260/c 691 bp mRNA linear EST 24-JAN-2002
 LOCUS BUI67260 full length cDNA library, chloronemata and young
 DEFINITION gametophores Physcomitrella patens subsp. patens cDNA clone
 pph14101.3', mRNA sequence.
 ACCESSION BUI67260 GI:18335242
 VERSION BUI67260.1
 KEYWORDS EST.
 SOURCE Physcomitrella patens subsp. patens.
 ORGANISM Physcomitrella patens subsp. patens
 Bui67260.1
 REFERENCE 1 (bases 1 to 691) Seki M., Kamiya A., Uchiyama, I., Nishiyama, T.,
 Fujita, T., Shin-I, T., Seki M., Kamiya A., Uchiyama, I., Nishiyama, T.,
 'Carninci, P., Hayashizaki, Y., Shimozaki, K., Kohara, Y. and Hasebe
 M.
 TITLE Comparison of the moss Physcomitrella patens genome with flowering
 plants genome
 JOURNAL Unpublished (2002)
 COMMENT Contact: Tadasu Shin-I
 Center for Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshin@genes.nig.ac.jp
 A backbone of the vector is basically from pBluescript(KS), that
 was in vivo excised from a modified lps phase vector (Mo bi Tec,
 Germany). 5' end of the cDNA that was digested with XhoI was
 ligated to SalI site of the vector and the 3' end including polyA
 tail was ligated to BamHI site of the vector. cDNA insert could be
 amplified with conventional T7 and T3 primers. This full-length
 cDNA library was generated basically according to the method
 described in the Plant J 15, 707-720 (1998) Seki M. et al.
 Protonemata were blended by the POLYTRON, and then cultivated on
 the BODAY medium for 13-14 days under the continuous light.
 location/Qualifiers
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 1. 691
 /organism="Physcomitrella patens subsp. patens"
 /db_xref="taxon:145481"
 /clone_lib="full length cDNA library, chloronemata and
 young gametophores"
 /tissue_type="mixture of chloronemata and young
 gametophores with 2 to 5 leaves"
 BASE COUNT 206 a 176 c 125 g 184 t
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 Query Match 12.7% Score 171.6; DB 10; Length 691;
 Best Local Similarity 58.1%; Pred. No. 9.9e-29;
 Matches 322; Conservative 0; Mismatches 229; Indels 3; Gaps 1;
 Oy 536 agaaagagatgtcagtcacacacagattgtgttcacatctgtgttct 595
 Db 691 AGAAGAAATCCACATCTCTTATGAGGTTTCGGCAGCATGATGGTGTACT 632

Oy 596 tgaacaaagattatcgtcgaaaaacgtgtgctcgaaagaacaaatgtgaatgtga 655
 Db 631 GG--ATGACGACGAAGAATCTCAAGAAAGATCGGGCTCGGAATTAACGTGTCACATGCA 575
 Oy 656 gaacaaagcctctacagattcctccagaacattatgtacacaaatgtgctta 715
 Db 574 CAAAGATCCCTTTTATACAGTTTATCAAGCGACATATCCAAATTCATCCATGATGAC 515
 Oy 716 agctcacttaactaagtcggaaggttccatcatgtctgtgggaatgtttagatt 775
 Db 514 GGTGGCCTGTGATGTCATGAGGTGATTTCTTACCTAATTTGGGCGATGCTTAAAGAT 455
 Oy 776 ggtgttatgttccatccatccatttcgctacacactcagattgttcataaaltggyggaag 835
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 Db 394 AAGCTGGAATACGGGTGATTTATCAAGAAATMACTGGTGGGTGACACTTCTTCATTTGG 335
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 Db 334 AGAAGTTGGCAACATACATACATGCTTTGAATATTCACCGAGCATGACTTGATG 275
 Oy 956 gtgacagatcgtatctgttgcgtatcagactcagactcagactatgttgatgtgtac 1015
 Db 274 GTGGCAGCTAGACCCCAACATGCTGATGATTTGTGCTTGAACCTGTGGAGTAGCTAC 215
 Oy 1016 caatgtgaagctacacactgaagctcagaagcaaaagctcagaagagtgcttaag 1075
 Db 214 AAGGTTAAAGCTCCGGAAGAAAGACACATGAGAGATTGACATTNATATTATTAAC 155
 Oy 1076 agtttgaagcatgt 1089
 Db 154 TTTTGGGGCTATGT 141
 RESULT 6
 AV442617 556 bp mRNA linear EST 14-NOV-2000
 LOCUS AV442617 Arabidopsis thaliana above-ground organ two to six-week
 DEFINITION Old Arabidopsis thaliana cDNA clone AP217b08_r 5', mRNA sequence.
 ACCESSION AV442617 GI:7613030
 VERSION AV442617.1
 KEYWORDS EST.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Arabidopsis thaliana: Streptophyta; Embryophyta; Tracheophyta;
 Eukaryota; Viridiplantae; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 556)
 Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
 A large scale analysis of cDNA in Arabidopsis thaliana: Generation
 of 12,028 non-redundant expressed sequence tags from normalized and
 size-selected cDNA libraries
 DNA Res. 7, 175-180 (2000)
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 /dev_stage="two to six-week old"

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XhoI"
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Best Local Similarity 61.4%; Pred. No. 8e-28;
Matches 307; Conservative 0; Mismatches 184; Indels 9; Gaps 2;

QY 189 cgaacatcagaagtcgtgttgagagaaatccaaagattctggccggaatgaac 248
DB 64 CCGCGCGCGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 123
QY 249 cctcgatatacaaaacgcgcacttaactgctcgaatgctctgcaagcagatg 308
DB 124 AGATTAAATATATGAAATCTCAGCTTCTTCACTGCTTCTCTCTCTCTCTCTCT 183
QY 309 cccttattcagcgtgagtcgcttgatctccttcttctcctgcttgcttgcaagc 368
DB 184 CCGTTTATTTCACCTTGCTGGGCTTGGGTTACGTTTGT-----TTACACCATC 237
QY 369 ggtgtcttgatcacttgctcctccatagatgcttactcagtcgagttcaagct 428
DB 238 GGTGCTCTGTGATCACCGCTCTTATCATCGCAACTGGCTCACCGAGTTTCAAGTTC 297
QY 429 cctaaagttggttagatctcttcttcttcttcttcttcttcttcttcttcttct 488
DB 298 CCTAAATGGCTTGAATCTCTTACCTTATGCTTATGCTTCTCTCTCTCTCTCTCT 357
QY 489 atggaatgggttagcaacacatagatcacacacagttcgatatacagaagaatgt 548
DB 358 ATTGATGGGTGATGATACATCGTTACCATCACAGTTCCAGATTTCAGAGATGATCCA 417
QY 549 catagtcacaactcaaggaatttgctctgctcactgattggtgtcttctgcaaaat 608
DB 418 CATAGTCCCTAAGAGAGCTTTTGTGATGATCTTCTTGTGATGATGATGATGATG 477
QY 609 ttcgtcgaaaaacgttggtcgcaagaacaaatgaaatgaaatgaaatgaaatg 668
DB 478 CTGTGTTTCAAA---GTGTGGAAGAGAGCAAAAGTGAGAGATTGAAAGGCAATGTTT 534
QY 669 tacagattcctccagaagaac 688
DB 535 TATAGGTTTCTTCGAAAC 554

RESULT 7
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LOCUS AV551184 Arabidopsis thaliana roots Columbia Arabidopsis thaliana
DEFINITION cDNA clone R2122d05R 5', mRNA sequence.
ACCESSION AV551184
VERSION AV551184.1 GI:8722597
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicots;
Rosidae; eudicots II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 552)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
DNA Res 7, 175-180 (2000)
20363093
JOURNAL Contact: Erika Asamizu
MEDLINE The First Laboratory for Plant Gene Research
COMMENT Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
FEATURES

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XhoI"
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Best Local Similarity 60.9%; Pred. No. 2.8e-26;
Matches 299; Conservative 0; Mismatches 183; Indels 9; Gaps 2;

QY 189 cgaacatcagaagtcgtgttgagagaaatccaaagattctggccggaatgaac 248
DB 71 CCGCGCGCGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 130
QY 249 cctcgatatacaaaacgcgcacttaactgctcgaatgctctgcaagcagatg 308
DB 131 AGATTAAATATATGAAATCTCAGCTTCTTCACTGCTTCTCTCTCTCTCTCTCT 190
QY 309 cccttattcagcgtgagtcgcttgatctccttcttctccttcttcttcttcttct 368
DB 191 CCGTTTATTTCACCTTGCTGGGCTTGGGTTACGTTTGT-----TTACACCATC 244
QY 369 ggtgtcttgatcacttgctcctccatagatgcttactcagtcgagttcaagct 428
DB 245 GGTGCTCTGTGATCACCGCTCTTATCATCGCAACTGGCTCACCGAGTTTCAAGTTC 304
QY 429 cctaaagttggttagatctcttcttcttcttcttcttcttcttcttcttcttct 488
DB 305 CCTAAATGGCTTGAATCTCTTACCTTATGCTTATGCTTCTCTCTCTCTCTCTCT 364
QY 489 atggaatgggttagcaacacatagatcacacacagttcgatatacagaagaatgt 548
DB 365 ATTGATGGGTGATGATACATCGTTACCATCACAGTTTCAGAGATGATGCCA 424
QY 549 catagtcacaactcaaggaatttgctctgctcactgattggtgtcttctgcaaaat 608
DB 425 CATAGTCCCTAAGAGAGCTTTTGTGATGATCTTCTTGTGATGATGATGATGATG 484
QY 609 ttcgtcgaaaaacgttggtcgcaagaacaaatgaaatgaaatgaaatgaaatg 668
DB 485 CTGTGTTTCAAA---GTGTGGAAGAGAGCAAAAGTGAGAGATTGAAAGGCAATGTTT 541
QY 669 tacagattcct 679
DB 542 TATAGGTTTCT 552

RESULT 8
B171184/c 680 bp mRNA linear EST 24-JAN-2002
LOCUS B171184 full length cDNA library, chloroplast and young
DEFINITION gametophores Physcomitrella patens subsp. patens cDNA clone
B171184 3', mRNA sequence.
ACCESSION B171184
VERSION B171184.1 GI:18339157
KEYWORDS EST.
SOURCE Physcomitrella patens subsp. patens.
ORGANISM Physcomitrella patens subsp. patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariaceae; Funariidae; Funariaceae; Physcomitrella.
1 (bases 1 to 680)
Fujiita, T., Shin-I, T., Seki, M., Kamiya, A., Uchiyama, I., Nishiyama, T.,
Carinci, P., Hayashizaki, Y., Shinozaki, K., Kohara, Y. and Hasebe
, M.
Comparison of the moss Physcomitrella patens genome with flowering
plants genome

```

**JOURNAL
COMMENT**

Unpublished (2002)
Contact: Tadasu Shin-
i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6836
Fax: 81-559-81-6835

Email: tshnige@genus.niig.ac.jp

A backbone of the vector is basically from pBluescript(KS), that was in vivo excised from a modified lps phage vector (Mo bi Rec, Germany). 5' end of the cDNA that was digested with XhoI was ligated to SalI site of the vector and the 3' end including polyA tail was ligated to BamHI site of the vector. cDNA insert could be amplified with conventional T7 and T3 primers. This full-length cDNA library was generated basically according to the method described in The Plant J 15, 707-720 (1998) Seki M. et al. Protonema were blenied by the POLYTRON, and then cultivated on the BCDYGA medium for 13-14 days under the continuous light.

FEATURES

```

/organism="Physcomitrella patens subsp. patens"
/db_xref="taxon:145481"
/clone="pph28c15"
/clone_lib="full length cDNA library, chloronemata and
young gametophores"
/listseq_type="mixture of chloronemata and young
gametophores with 2 to 5 leaves"
BASE COUNT      150 a      246 c      122 g      162 t
ORIGIN

```

[illegible]

RESULT 9

LOCUS	AV550066	513 bp	mRNA	linear	EST 06-SEP-2006
DEFINITION	AV550066 Arabidopsis thaliana roots Columbia Arabidopsis thaliana				
ACCESSION	cdna clone R2107g08R 5', mRNA sequence.				
VERSION	AV550066				
KEYWORDS	AV550066.1	GI:8721479			
SOURCE	EST.				
ORGANISM	thale cress.				
	Arabidopsis thaliana				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.				

REFERENCE
AUTHORS
TITLE

1 (bases 1 to 513)
Asanizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in *Arabidopsis thaliana*: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)

JOURNAL
MEDLINE
COMMENT

Contact: Zhang, Xianming
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizuka@kazusa.or.jp, URL: <http://www.kazusa.or.jp/en/plant/>

FEATURES
SOUND

```

/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="R2107908R"
/clone_id="Arabidopsis thaliana roots Columbia"
/tissue_type="roots"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2
XhoI"

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Best Local	Similarity	60.4%	Pred. Num 1.9e-24		
Matches	272	Conservative	0	Mismatches 172	Indels 6
					Gaps 1
189	cggacatcagaagtcgltgttggagaagaatccaaagatctctgcgcccgaatggaac	248			
66	ccggcggcgcggtgagagagaagaagagacatggctgtttggagatggaagtgagacg	125			
249	cctcgtgatattcaaaaagcgctacttaactacggtccatcgtctcagtcctcagcagatgagcg	308			
126	agattagattatgtgaaatttcacgcttctttcacggttcatttcttctctcttgggt	185			
309	cccttattatcagctcgtggatcgttttggatctcttatacttgcgttgcgaacg	368			
186	ccgttttttttccactggcgcgcgccttttgggttttgcctttttgtt-----ttacacacac	239			
369	gagtcctctggatatacacttttggctccatagatgcttcaactaagtcgagtttcaagctt	428			
240	gggtgctttgttgatccacgcctctctttttatccatccgaacttggcttcacggagtttcaaaagtc	299			
429	ccctaagtttgttgaactactcttgcctactcgtgtgctctctgcctctcaaggagatccc	488			
300	cctaaatggccttgatgattctcttagcccttattgtgccccttctgcctttttagggagatccg	359			
489	atggaatgggttgagcaaccatagatcacatcacccagtttgcgtatcacgaagaagatgctt	548			
360	attgatttggtgtgagtcacacatccctttaccatccacagtttccagatttcagaaactgattcca	419			
549	catagttccaactaaagagatttggctctgtacacatttggttgggttcttgacaaagattta	608			
420	catagttccataggaagaaggttttggtttagcattcttggattatgactcttgcctatt	479			
609	ttcgtcgaanaaagctgtggtgcgaagaac	638			
480	cttggtttcaaatgttgcaagaagaagcaaac	509			

LOCUS
DEFINITION

[illegible]


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BASE COUNT      210 a      159 c      99 g      161 t
ORIGIN
```

Query Match	11.2%	Score 152.4	DB 9	Length 629
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QY	625	gTggcgcgaagaacaacatgtaatagtattgtaagaagaacaagccctctacagatccctccaga	684	
Db	601	GTGAGAGAGAGCAAAACCTGGAGGATTGTGAAGAGCAGCATGGTTTATAGGTTCTTTCAGA	542	
QY	685	aaacttaatagtacacatcaatctgctcctaatagcctctactactaagtcggaggttc	744	
Db	541	AAACAGTGCCTATTTTCACATTTTATGAGATTGGCTTTCTTCTCTTCACTTGGTGGCAAGT	482	
QY	745	catacatgctcTggggaaTgggtctctagatctggtctatgctctatgctccatccattgcgtca	804	
Db	481	CCTTGCCTACTTGGGGCAATGGGGGATGAGGAGCAGCATTTGGAGTGCACCTGACTTCCCTCA	422	
QY	805	tcaactcaagcttctgcataaataatTggggcggaaagccatgtaatactgaggaattatccagcca	864	
Db	421	TAAATTCACCTCTGGCATTCTTTGGGGCACTCCCAACATCTGGAGAACCAATATACACTTCTCGTA	362	
QY	865	acaaatactctgctgcattgctcattgctctgtttggaagggctctgcataaapacacacacagcat	924	
Db	361	ATGTTTGGTGGTTATTCGGTATTTTTCATTTTGGAGAGAGTGGCAACAAATCATCTCATGSGCT	302	
QY	925	tgcgaacaatccatccctgcgaacaacgggctcagaatggttggcagatcgatctgtaactgtaactgta	984	
Db	301	TTCGAGTCATTCGGCTTAGACAAAGCAGCTTGAAATGTTGGCAATAATTCCTTGATGATCATTTG	242	
QY	985	tcaagagctctcaagaactatggaattgctgctccaatgtaagaactcaacaactgaaagctca	1042	
Db	241	TTTCGGTTTTCGAAATATATTCGGTTTATGCGACCGATGTGTAATGAATGGTCCCAACGGGAGGCTCA	184	

RESULT	11
AV550487	
LOCUS	522 bp mRNA linear EST 06-SEP-2000
DEFINITION	AV550487 Arabidopsis thaliana roots Columbia Arabidopsis thaliana
ACCESSION	CDNA clone R2113b04r 5' mRNA sequence.
VERSION	AV550487
KEYWORDS	AV550487.1 GI:8721900
SOURCE	EST.
	thale cress.

BASE COUNT	ORIGIN
127 a	103 c 134 g 158 t

	Best Local Similarity	61.1%	Pred. No. 2.5e-24;		Length 22e.	
	Matches 266;	Conservative	0;	Mismatches 165;	Indels 6;	Gaps 1;
QY	204	gctgtgagagaaatccaaaggatctcggccggaatgaaacctcgtatctcaa	263			
Db	90	GAGAGAGAGAGAGAGATGGGTCTTTGGATAGAAAGTGGAGAGATAGATATATGTG	149			
QY	264	aagcgcgtcacttctcgtgctcgtcaatcgtcttcgacgcatgagcgcccttatttcagc	323			
Db	150	AAATTCCTCAGCTCTTTTACAGTGTTCATATTCCTCTGGCTCCTTGGCCCTCTTATTTTACCT	209			
QY	324	tggagatcgatttggatcctcttattccttgcgttggcttcgcaagcggtcttcttgatc	383			
Db	210	TGGTGGCTCTTTGGGTTACGTTTTGTT-----TTACACCATGGGTGGCTTGGTATC	263			
QY	384	actttgctctccatagatgctcttactcaatcggcgtttccaagcttcctcaatctggtttag	443			
Db	264	ACCGCTCTTATCATCGCAACTTGGCTCACGGAGATTCCAAGTCTCTTAATGGCTTGAG	323			
QY	444	tactcttctgctactgctggtctctctgctctcttcaggagatcccatggaatgggttagc	503			
Db	324	TATCTCTTAGCCTATTTGGCCCTTCTCCCTATTCAGGGAGATCCCATTTGATTTGGGTGAGT	383			
QY	504	aacacaaagtaacacacacagcttcgtcgatccagaagaagaatgtctcatagtcacaactcaa	563			
Db	384	ACAACATGCTTACCATCACACAGTTTCACGAGATTTCAGAACCTGATCCCATATAGTCTTAAAGAA	443			
QY	564	ggattctggtctcgtcacatctggttgggtctcttgacaagaatttatctgcgcgaaaaacgt	623			
Db	444	GGTATTTGGTTAGCATCTTCTTGGATCATATGACTCTGCCTATCTTGTTCANNAAGTGT	503			

DB	504	CGACAGACGACCAAC	518
RESULT	12		
AI993202			
LOCUS	AI993202	494 bp	mRNA
DEFINITION	701495686 A. thaliana, Ohio State clone	set	linear EST 08-SEP-1999
ACCESSION	AT993202	CDNA clone 701495686,	mRNA sequence.

VERSION	AI993202.1	GI:5840107
KEYWORDS	EST.	
SOURCE	thaie cress.	
ORGANISM	Arabidopsis thaliana	
REFERENCE	Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.	
AUTHORS	1 (bases 1 to 494) Chen J., Momiyana, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D., Wang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P., Gorgone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D., Tan, R., Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C., Carpio, T., Policky, J., Suzuki, G., Argentine, C., Shah, S., Nobriga, A., Murry, L., Turner, C., Kirkorian, S., Elder, L. and Hanson, D.	
TITLE	Arabidopsis thaliana Gene Expression Microarray Unpublished (1999)	
JOURNAL	Contact: David Smoller, Ph.D. Genome Systems, Inc., a wholly owned subsidiary of Inocyte Pharmaceuticals, Inc.	
COMMENT	4633 World Parkway Circle, St. Louis, MO 63134, USA Tel.: 877-577-2733 Fax: 314-427-3324 Email: service@genomesystems.com.	
FEATURES	Location/Qualifiers	
SOURCE	1..494 /organism="Arabidopsis thaliana" /db_xref="taxon:3702" /clone="701495686" /clone.lib="A. thaliana, Ohio State clone set" /note="cdNA library was made from selected clones from the Arabidopsis thaliana Ohio State clone set."	
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ORIGIN		
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Best Local Similarity	60.6%: Pred No. 4.3e-22;	
Matches 269; Conservative 0; Mismatches 171; Indels 4; Gaps 2;		
OY 374	tcttgatcacttgtgctccacagtgcttcatacatgycgtttcaacagtcca 433	
Dd 49	TTCTTAGCATTAATTTTCATACATAGGAAGTGTGACTGCACAAGACTTTAAAGCTTCCTAA 108	
OY 434	gttgtgtgtaactctcttgcctaetgtgtgctctctgccttcagggaagatccaatgga 493	
Dd 109	ATGGCTTAAATAATCCATTGCGCTTATTCGCCCTTTCCGCTTGAGGGGTCAATCATAATGA 168	
OY 494	atgggtgacaaccatagatgccaccacacagttctgtcacagaagaagatgttccatag 553	
Dd 169	TTGGGTGATACACATPAGGTTCCATCACACAGTTCACAAATTCAGACCCTGACCCCACATAG 228	
OY 554	tccaactcaaggatttggctctgtcacatgtgttggttgccttgacaagaatttatcg 613	
Dd 229	TTCATTCGAAGAAGATTCTGTTGATGACAGCTGTTTTGATATTCAGATTCACACACAGTTACATAG 288	
OY 614	cgaaaaagctgtggtgcgaagaagaacaaagttaatatatttgaaagaagaaccttcacag 673	
Dd 289	AGAAAAGTGTGAG---GACGTGACAAAGTGTGAGACTTTGAACAAATGAGTTTATATAG 345	
OY 674	atctctcagaanaactatattgatcatcaaatgtgctctaaatagcttacttactaagt 733	
Dd 346	GTTTCTTCGAAAAACAAATGGTGGTCTCCACATPCTTAACATTTTGGACCCCTGCTATTTATAT 405	
OY 734	cggagggttccatcatatgtctcggggagatgggtttagattgtgtttaagttcaltc 793	
Dd 406	GGGGTGCTTACCTTAC--TAACCTTTCGGCTGGGTGCTTGAGAGAAAAATCGGTTACAAATGG 464	
OY 794	caattcgtcatacaactcagtttg 817	
Dd 465	GACCTTGCCCATTAACCTGCGCATG 488	
RESULT	13	

[illegible]

Oy	555	caccaccaagaatttgatcttgcctcactggttgagtcctcgaca	600
Dd	561	CCTTATGAAGGATTGTGGTCACGTCAATGAGTGGAATTTGATA	606
RESULT	14		
LOCUS	B1931427	721 bp	mRNA linear EST 18-OCT-2001
DEFINITION	EST551316 tomato flower, 8 mm to preanthesis buds Lycopersicon esculentum cDNA clone cTCC20C17 5' end, mRNA sequence.		
ACCESSION	B1931427		
VERSION	B1931427.1	GI:16245899	
KEYWORDS	EST.		
SOURCE	tomato.		
ORGANISM	Lycopersicon esculentum		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;		
AUTHORS	Lycopersicon. van der Hoeven,R.S., Bezzerides,J.L., Karamychava,S.A., Tsai,T.J., Utterback,T., Van Aken,S., Romling,C.M., Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.C. and Tanksley,S.D. Generation of ESTs from tomato flower tissue, buds 8 mm - preanthesis Unpublished (2001) Contact: CUGI Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Email: http://www.genome.clemson.edu/orders/index.html This clone is available through the Clemson University Genomics Institute Seq primer: T3. Location/Oualifiers 1..721 /organism="Lycopersicon esculentum" /cultivar="TA496" /db_xref="taxon:4081" /clone="cTCC20C17" /clone_1lb="tomato flower, 8 mm to preanthesis buds" /tissue_type="flower" /dev_stage="buds 8mm to preanthesis" /note="Vector: pBluescript SK(-); Site1: EcoRI; Site2: XhoI; supplier: Cornell University; sequencing: The Institute for Genomic Research; Flower buds and flowers were taken from greenhouse plants (4-8 wks old, TA496). They were immediately frozen in liquid nitrogen and then size-separated while remaining frozen."		
JOURNAL			
COMMENT			
TITLE			
FEATURES			
SOURCE			
BASE COUNT	196 a 150 c 160 g 215 t		
ORIGIN			
Query Match	10.5%; Score 142; DB 10; Length 721;		
Best Local Similarity	61.1%; Pred. No. 5.3e-22;		
Matches 248; Conservative	0; Mismatches 155; Indels 3; Gaps 1;		
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Dd	297	TCTGATGATGTCGTGACCCGCCCTTAGGATGTGCTTGGGGAAGCAATTCATTCATG	356
Oy	255	gataatccaagaacgcgcctaacttaactgacctgcatgctctgcagcgatggcgccctt	314
Dd	357	GATATGGCTCAGCGTGGCGGTGTGTGTCATTCATTCATTCATTCATTCATTCATTC	416
Oy	315	tatttcagctgggatcgcttttgatctcttcaactctgctggatctgcgaacgctggt	374
Dd	417	ACTTTCATTCAGCTGCTCTTGGGATTCATTCATTCATTCATTCATTCATTCATTC	473
Oy	375	cttgttatcaactctgtcttccatagatgcttctactacatggcgtttcaagctcctaag	434
Dd	474	CTCGGCTATTCACACTTCTTTTACACAGAACCCTCTCATTAAGATTTCAAACTTCCCAA	533

Oy	435	tggcttggaagactcttctgacactcgttcgtccgtcttcaggaaagtccatgtgaa	494
Dd	534	TGGCTTGGAAGACTCTTCTGACACTCGTTCGTCCGTCTTCAGGAAGTCCATGTGAT	593
Oy	495	tgggttagcaaccatatgataccatcaccaagtcgtcgatatacagaagaagatgtcatagt	554
Dd	594	TGGGTTAGCAACCATATGATAGGTAACCAACATCACTTTGTGCATTACAGAAGAACCCACAGT	653
Oy	555	ccaaccacaaggaatttgtgtctgtctacacatcgttgtggtttcttgaca	600
Dd	654	CCTTATGAAGGATTTGGTTGGTCACTCATATGACATGGGATTTGTGATA	699
RESULT	15		
LOCUS	B1997512	660 bp	mRNA linear EST 25-OCT-2000
DEFINITION	1031050C07.y2 C. reinhardtii CC-1690, Stress II (normalized), lambda zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.		
ACCESSION	B1997512		
VERSION	B1997512.1		
KEYWORDS	EST		
SOURCE	Chlamydomonas reinhardtii.		
ORGANISM	Chlamydomonas reinhardtii Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadales; Chlamydomonas.		
REFERENCE	Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C., Lefebvre, P., McDermott,U.P., Shrager,J., Silflow,C. and Stern,D. Analysis of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants. Project: 1031 Unpublished (2001)		
AUTHORS	Contact: Charles Hauser DCMB Box 91000 Duke University Durham, NC 27708-1000 Tel: 919 613 8159 Fax: 919 613 8177 Email: chauser@duke.edu		
JOURNAL			
COMMENT			
FEATURES			
source	Location/Qualifiers 1..660 /organism="Chlamydomonas reinhardtii" /strain="CC-1690 wild type mt+ 21gr" /db_xref="taxon:3055" /clone.lib="C. reinhardtii CC-1690, Stress II (normalized)), lambda zap II." /note="Vector: pBluescript II SK-; Site.1: EcoRI; Site.2: XhoI; Stress condition II library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (NH4+ - containing) and shifted to TAP - NO3-(24hrs); H2 production conditions (0, 12hr, 24hr) see Wells et al.,(2000) Plant Phys. 122: 127-135; TAP + H2O2 (1, 12, 24 hr); TAP + sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr). POLYA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda zap II (Stratagene) in the EcoRI (5') and XhoI (3') sites. pBluescript II SK+ plasmids were excised from the lambda ZAP clones by superinfection with Exsistist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806."		
BASE COUNT	106 a 211 c 223 g 120 t		
ORIGIN			
Query Match	10.5%; Score 141.8; DB 10; Length 660;		
Best Local Similarity	58.8%; Pred.No. 5.9e-22;		
Matches 245; Conservative 0; Mismatches 172; Indels 0; Gaps 0;			
638 caaatgtgaatgatattggaacaacgcctctacagatctctcagaaaccttatatgta	697		

```

Db 41 CAACGGGACGACCTGGAGAGCAGTGTACTACCGCTGGCTGGCGAGACCTACCCCTT 100
QY 698 ccataattggtcttaataagcttaacttaacttaacttaacttaacttaacttaactta 757
Db 101 CCATGTGGCTGCTCAGCTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 160
QY 758 gggaaatgggtttagatgggtttagatgggtttagatgggtttagatgggtttagatgggtt 817
Db 161 GGGTGGCGCGCTGGCGCATGTGCTGGCGCATGTGCTGGCGCATGTGCTGGCGCATGTGCTG 220
QY 818 tcataaatggggcggaagggcgaatgggaatgggaatgggaatgggaatgggaatgggaat 877
Db 221 GCACTGCTGGGGCTACCAAGGACTACCAACCGGCGACCTGTGGAAGAACAACTGGTGGGT 280
QY 878 tgcattgtgtcgttttgagaggggtgacataaacacacacacacacacacacacacacac 937
Db 281 GGGCATCTGGGCTTTGGGAGGGGCTGGCACACCAACCGGCGCTGTGAGTTCTTCTGC 340
QY 938 tcgacacgggctagaatgggtgacagatcgatgttactgtgtactgtgtactgtgtactgt 997
Db 341 GCGCCACGGCTTCAGTGTGTGGCAAGTGTGACATGACCTGTGATCATCTGTGGCTCTCCA 400
QY 998 agctattggtgctaccgaatggaagctacgaactgaagctgaagctgaagctgaagctga 1054
Db 401 GAAGGTGGGCTGGCGCACCAAGTGAAGTGTGCCACGGAGCGCGCGAAGGCCAAAGCT 457

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Search completed: September 13, 2002, 08:11:11
 Job time: 5536 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2002, 08:45:51 ; Search time 61.47 Seconds

(without alignments)
643.278 Million cell updates/sec

Title: us-09-664-840-2

Perfect score: 1946

Sequence: 1 LRSLYRPPISISLSLEAM.....ATNWKLEAKOKRKAASA 356

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

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6: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1946	100.0	356	20	AAV39361
2	978.5	50.3	371	21	AAAG39561
3	969.5	49.8	371	21	AAAG21191
4	967.5	49.7	293	21	AAAG39562
5	958.5	49.3	293	21	AAAG21192
6	930	47.8	360	21	AAAG19661
7	930	47.8	361	21	AAAG19660
8	929	47.7	271	21	AAAG39563
9	920	44.9	307	21	AAAG21193
10	874.5	44.9	307	21	AAAG51215
11	874.5	44.9	326	21	AAAG51215

12	872	44.8	308	21	AAAG09499
13	872	44.8	327	21	AAAG09498
14	870.5	44.7	311	21	AAAG30599
15	788.5	40.5	300	21	AAAG21186
16	785.5	40.4	299	21	AAAG22905
17	785.5	40.4	313	21	AAAG22905
18	780.5	40.1	282	21	AAAG21187
19	771	39.6	309	21	AAAG09773
20	767.5	39.4	299	21	AAAG09774
21	689	35.4	272	16	AAAR76811
22	687	35.3	272	16	AAAR70260
23	650	33.4	318	16	AAAR70259
24	588.5	30.2	192	21	AAAG21188
25	556	28.6	278	16	AAAR76810
26	486.5	25.0	181	21	AAAG12679
27	484.5	24.9	160	21	AAAG12681
28	484.5	24.9	167	21	AAAG12680
29	367	18.9	128	21	AAAG16042
30	366.5	18.8	384	22	AAAB71665
31	359.5	18.5	461	22	AAAB64635
32	359	18.4	451	19	AAAW51087
33	354	18.2	445	19	AAAW70099
34	351.5	18.1	383	22	AAAB65786
35	351.5	18.1	383	22	AAAB66209
36	351.5	18.1	383	22	AAAB66210
37	351.5	18.1	383	22	AAAB71402
38	342.5	17.6	359	21	AAAB69378
39	342.5	17.6	359	22	AAAB44583
40	342	17.6	354	13	AAAR25853
41	336.5	17.3	359	21	AAAY69377
42	335	17.2	330	22	AAAG63850
43	335	17.2	330	22	AAAG63934
44	335	17.2	330	22	AAAG63225
45	329.5	16.9	358	22	AAAB44582

ALIGNMENTS

RESULT 1	
AAV39361	
ID	AAV39361 standard; Protein: 356 AA.
XX	
AC	AAV39361;
XX	
DT	20-DEC-1999 (first entry)
XX	
DE	Delta-5 acyl-CoA desaturase.
XX	
KW	Delta-5 acyl-CoA desaturase; double bond; plant membrane; neutral lipid;
KW	seed tissue; palmitoyl-CoA; oleoyl-CoA; fatty acid elongase; biopolymer;
KW	biosynthetic pathway; lubricant; grease; plastic; ink; cosmetic;
KW	surfactant; biodegrade; long shelf life.
XX	
OS	Limonches douglasi.
XX	
PN	WO9949050-A2.
XX	
PD	30-SEP-1999.
XX	
PF	12-MAR-1999; 99MO-US05471.
XX	
PR	20-MAR-1998; 98US-0078736.
XX	
PA	(DUPO) DU PONT DE NEMOURS & CO E. I.
XX	
PI	Cahoon EB, Hiltz WD, Kinney AJ, Vollmer SJ;
XX	
DR	WPI: 1999-591101/50.
DR	N-PDB; AA28315.
XX	
PT	Nucleic acid fragments useful in the production of industrial agents
PT	for eg. lubricants or cosmetics -

XX Claim 1; Page 46-47; 54pp; English.
 PS This is the amino acid sequence of the Limnanthes douglasii delta-5
 CC acyl-CoA desaturase. Delta-5 desaturase introduces a double bond at the
 CC delta 5 position of a C20 fatty acid. Delta-5 desaturase is an enzyme
 CC which is able to further desaturate mono-unsaturated fatty acids to make
 CC poly-unsaturated fatty acids. Fatty acids are used in plant membranes
 CC and in neutral lipids that are formed for the storage of energy in
 CC developing seed tissue. The delta-5 desaturase nucleotide sequence can be
 CC linked to regulatory sequences and used to transform host cells. The
 CC invention also reveals a fatty acyl-CoA elongase amino acid sequence
 CC (AAV39362), this enzyme prefers palmitoyl-CoA (16:0-CoA) as its substrate
 CC instead of oleoyl-CoA (18:1-CoA) the usual substrate for the known plant
 CC fatty acid elongase. The nucleic acid sequences of the delta-5 desaturase
 CC and the acyl-CoA elongase can be used in genetic engineering to
 CC manipulate fatty acid biosynthetic pathways, allowing changes to be made
 CC in the fatty acid composition of plants and or oils and to introduce new
 CC pathways in to oil seeds in order to produce new biopolymers from
 CC acyl-CoA. The oils and fatty acids produced by the genetically engineered
 CC plants have potential for use as industrial agents including lubricants,
 CC greases, plastics, inks, cosmetics and surfactants. Polyestolides derived
 CC from the 20:1 delta-5 fatty acids of Limnanthes biodegrade slower than
 CC those derived from soybean oils or oleic oils, and thus will produce
 CC industrial products with a longer shelf life.
 CC
 XX Sequence 356 AA;

Query Match 100.0%; Score 1946; DB 20; Length 356;
 Best Local Similarity 100.0%; Pred. No. 2,1e-197;
 Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRLSLYPTISISLSISLRLAMASFIATTPPAMPAPASVLDPKIPKPEKTEPRKPDLE 60
 Db 1 LrlslYptIsIsIsIsLrlaMasfiAtTpPaMpApASvldPkIpKpEkTePrKpDle 60
 QY 61 RPRISVVLERSKSGFMRKRNPRDIONAVTLVLHALAAMAFYSWDAEWISFLLGF 120
 Db 61 RPrISvVLERsKSGfMRkRNpRDIONaVTLvLHALaAMaFYsWDAeWISfLLGF 120
 QY 121 ASGVGILCFRCLTHGSGFKPLVEYEFACGSLALOGDPMENVNHRVHNOVDPR 180
 Db 121 aSgvGiLcFRclThGsgfKPlVeYEFaCGsLaLoGDpMeNvNhrVhNoVdPr 180
 QY 181 DVHSPTQGFMCNIGWVLDKDLFEKRGGRNNVNDLKKQAFYRFLQKTYMHQALATL 240
 Db 181 dVhSpTqGfMcNiGwVldKdLfEkRGgRnNvNdLkKQaFYrFlQkTyMhQaLaTl 240
 QY 241 LYYVGFYIYWGKGFRLVPEHSTFAINSVCHKKGRRPNTGDSITNNMFYALCAFGEG 300
 Db 241 lYyVgFYiYwGkGfRlVpEHsTfAiNsVcHkKgRrPnTgDsITnNmFYaLcAFgEg 300
 QY 301 WHNNHAFEOSARHGLEMMWQIDVTWYVIRTLQALIGLATNVKLPTPAOKOKLKAKSA 356
 Db 301 whnnHafEoSARhGLEmMwQIdVtWYvIRtLQaLiGLaTnVklPtPaOkOkLkAkSa 356

RESULT 2
 AAG39561
 ID AAG39561 standard; Protein: 371 AA.
 XX AAG39561;
 AC
 XX 18-OCT-2000 (first entry)
 DT
 XX Arabidopsis thaliana protein fragment SEQ ID NO: 48968.
 DE
 XX Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX
 OS Arabidopsis thaliana.

XX EP1033405-A2.
 PN 06-SEP-2000.
 XX
 PD 25-FEB-2000; 2000EP-0301439.
 XX
 PR 25-FEB-1999; 99US-0121825.
 PR 05-MAR-1999; 99US-0123180.
 PR 09-MAR-1999; 99US-0123548.
 PR 23-MAR-1999; 99US-0125788.
 PR 25-MAR-1999; 99US-0126264.
 PR 29-MAR-1999; 99US-0126785.
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 PR 06-APR-1999; 99US-0128234.
 PR 08-APR-1999; 99US-0128714.
 PR 16-APR-1999; 99US-0129845.
 PR 19-APR-1999; 99US-0130077.
 PR 21-APR-1999; 99US-0130449.
 PR 23-APR-1999; 99US-0130510.
 PR 23-APR-1999; 99US-0130891.
 PR 28-APR-1999; 99US-0131449.
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 PR 30-APR-1999; 99US-0132407.
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PR	26-OCT-1999	99US-0161360
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PR	28-OCT-1999	99US-0161926
PR	28-OCT-1999	99US-0161992
PR	28-OCT-1999	99US-0162142
PR	29-OCT-1999	99US-0162143

Query Match	50.3%;	Score 978.5;	DB 21;	Length 371;
Best Local Similarity	56.2%;	Pred. No. 6.7e-95;		
Matches 173;	Conservative 52;	Mismatches 80;	Indels 3;	Gaps 3;

QY	45	KPERKTEPRKDKDLERNPTSEUULVERKSK-GFWRRKKNNPRDIONAVTLVLVNLAMAR	1030
Db	61	krdyttaaateagdyttimlsvdvtkkkkkkkvwwewekamdfgavayvlsmbllslar	1200
QY	104	FVFSWDAFWISFILLGFASGVLTGTFEHRCLTGHGKRLPRVLVFPFAYVGSJALOGDPM	1630
Db	121	fgfnvtaavsvfgy-lvtglllgltcltfbhrnlshkafkrlpwleyllaqsqaqlqgnrl	1790
QY	164	EMVSNHRYNHOFTVTERDVNSPTOGFWFNCISGNWLDLDLEVEKKRGRRNNVNDLKOAFY	2230
Db	180	dwtavethryhbfcsddrphrslrgfwfshmmwfdctc-ltqcgserpnvgdlekqrfy	2280
QY	224	RFLQKTYVYHODALLALLYUGGFRPYLVWGSGRVLVEMHSTEAINSVCKHKGSGRPWNTG	2630
Db	239	rflcttyyllhrblaalavaluamgqfrflwvgyvrlvuvyhlvtwlvnsachvwgkqewntg	2980
QY	284	DLSTNNKVVALCAFGEGNNNNNNHNFEOASAKRGLEEMWODIDTWTYKTLQALGLATNVKLR	3430
Db	299	disknnwvaalaigevghnbnhafeisatqtlewgdldmtwvuvkflqadlglatdvykr	3580
QY	344	TEAQOKOL 351	
Db	359	seaqkqzm 366	
RESULT	3		
NAAG21191			

ID	AG21191 standard; Protein: 371 AA.
XX	
AC	AG21191;
XX	
DT	17-OCT-2000 (first entry)
XX	
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 23657.
XX	
KW	Protein identification; signal transduction pathway; metabolic pathway;
KW	hybridisation assay; genetic mapping; gene expression control; promoter;
KW	termination sequence.
XX	
OS	Arabidopsis thaliana.
XX	
PN	EP1033405-A2.
XX	
PD	06-SEP-2000.
XX	
FE	25-FEB-2000; 2000EP-0301439.
XX	
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OY 145 LVVEYFAVCGSLALQGDPMEMVSNHRYHNOFVTERDVHNSPTQGFMCNIGWLDKDLFV 204
DB 61 wleylleyogaeqlqgnrldlwsrlthynqfcdsdtdrpsrldqfwsfmmnmfdltnt-1 119
OY 205 EKRGRNNVNDLKKQAFYREFLOKTYMYHQLALALLVYVGFRPYLVWGMGFRILVFMFHS 264
DB 120 lqrcgepnvngdlckprfryflrtctyllhplalavalymgfrflvwgmgnvllvvvyl 179
OY 265 TFAINSVCHIKMGSRPNWTGDLSTNNMFVALCAFEGCGHNNHNAFEQSARHGLEWMOIDVT 344
DB 180 lwlvnaschhwgqawltcdlsknwvaalafgegwhnnhhafefsarhglewqldmt 239
OY 325 WYVIRTLQALIGLATNWKLPTEAKOKL 351
DB 240 wyyvkkflqalqldatdklpsaaqkqcm 266

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XX
AC AMG21193;

XX
DT 17-OCT-2000 (first entry)

XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 23659.

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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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AC AAG51216;
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 64979.
KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
XX
XX Arabidopsis thaliana.
PM EPI033405-A2.
XX
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XX
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Best Local Similarity 52.4%; Pred. No. 5.3e-84;

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OY 122 SCVIGILCHRCITHGEGFLPKLYEYEFAYCGSLAQDPMEMWVSHRRYHOFVDERD 181
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OY 182 VHSPTQGFWFCIHGWLDKDLFEKRGKRRNNVNDLKKQAFYRFLOKTYMHOLALIAL 241
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RESULT 11

AA051215 standard; Protein; 326 AA.

AA051215;

18-OCT-2000 (first entry)

Arabidopsis thaliana protein fragment SEQ ID NO: 64978.

Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.

Arabidopsis thaliana.

EP1033405-A2.

06-SEP-2000.

25-FEB-2000; 2000EP-0301439.

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 PR 22-OCT-1999; 99US-0160980.
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Query Match 44.98; Score 874.5; DB 21; Length 326;
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 Oy 64 TSEVLEKRSKG--FWRRKNPNDIONAVTLVLHAAAMAPEVFSMAFISITLGA 121
 Db 36 tpaaveekkttrwfwdrirrrllyvkrtsastvnslllepfyftwaaawtllf--yt 93

Query Match	44.8%	Score 872	DB 21	Length 308
Best Local Similarity	52.2%	Pred. No. 9,9e-84		
Matches 152	Conservative 45	Mismatches 88	Indels 6	Gaps 3
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DB	17 tpaaeeekkkrrtwwfwtdrtwrlidyykffsafsftvshlalllapyftwsalwvflf--y	74		
OY	121 ASVLGILTCFHCRLCTHGGFRLPRLVEXYFAVCGSLALOGDPMEMVNNRYHNOFVTER	180		
DB	75 tlgsgltvsvyhrhlahrsfkvrkwlleyllaycallalqgrldweshryhghftser	134		
OY	181 DVHSTOGFEWCHGMYLDKDLFEYKKGGRNNVNDLKQAFYFLQKTYMHOLALIAL	240		
DB	135 dphprkqewfshlwlwydsaylvsk-cgrtaavedlkrqwyfllqktvlfhllgiff	193		
OY	241 LVYVGGRPYIVMGNGFRLVEMFHSFPAINSVCHKMGGRPNWTCGLSTNNMFVALCARGEG	300		
DB	194 lfyjgsmfsvlwmvgvgaalelhtcllnschlwgctcktkndtsrnnvwslvstges	253		
OY	301 WHNNHHAFCOSARHGLEWQJIDVTWYVIRTLQALIGLATNPKLPTDAOKRL	351		
DB	254 whnnhkfksaarglwwgqldiswyivrrffellglatdvkvrpeagrrm	304		
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AC	AAAG09498;			
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DT	17-OCT-2000 (first entry)			
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DE	Arabidopsis thaliana protein fragment SEQ ID NO: 7457.			
KM	Protein identification; signal transduction pathway; metabolic pathway;			
KW	hybridisation assay; genetic mapping; gene expression control; promoter;			
KM	termination sequence.			
XX				
OS	Arabidopsis thaliana.			
PN	EP1033405-A2.			
XX				
PD	06-SEP-2000.			
XX				
PF	25-FEB-2000; 2000EP-0301439.			
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PR	25-MAR-1999; 99US-0121825.			
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PR	08-APR-1999; 99US-0128714.			
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Query Match 44.88; Score 872; DB 21; Length 327;
Best Local Similarity 52.28; Pred. No. 1,1e-83;
Matches 152; Conservative 45; Mismatches 88; Indels 6; Gaps 3;

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DB lpaaveeekkkrrwfwdrtridvkvfsasfchsalalapyfksalwvtfllf-y 93
OY 121 ASGVGIRLCPRCLTHGCFRLPKLVEFFAYCGSLAQDPMWVSNNRHHQFVPTER 180
DB 94 tlg9dltvbyhrnlshsfkvpxwleyllaqcdldwvachryhqbftdser 153
OY 181 DVHSPTQCFMFCIHGWLKDLFEKRGGRNNVNDLKAQAFYRFLQKTYMHQALIAL 240
DB 154 dphapkegfwfshllwlydsaylvsk-cgrtanvedlkrtqfyfllqkcvlfhllgiff 212
OY 241 LYYGCGPRYITWGMGFRLEVNFHSTFALINSVCHKMGGRPNNTGDLSTNNFVALCARGEG 300
DB 213 lfyigmstfvmgvgaaelhvtclnslchlwtgtrctktdtstnvwvlsfsges 272
OY 301 WHNNHAFPEOSARHGLFEMWQIDVWYVIRTLQALIGLATNKKLPFEAKOKL 351
DB 273 whnnhafsaaarglewqdlswylvrfellglatdvkpldaqrirm 323

RESULT 14

AAG30599

ID AAG30599 standard; protein; 311 AA.

XX AAG30599;

XX 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 36610.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX Arabidopsis thaliana.

PN EP1033405-A2.

XX 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

XX 23-MAR-1999; 99US-0125788.

XX 25-MAR-1999; 99US-0126264.

XX 29-MAR-1999; 99US-0126785.

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XX 06-APR-1999; 99US-0128234.

XX 08-APR-1999; 99US-0128714.

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PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151308.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155559.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.

PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0158294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 40.5%; Score 788.5; DB 21; Length 300;

Best Local Similarity 50.2%; Pred. No. 6.6e-75; Matches 144; Conservative 46; Mismatches 94; Indels 3; Gaps 2;

OY 65 SEVLEERSKGFWRKRNPRDIONAVTLLVLAALAMAFYFSDAFWISFILLGFASGV 124
DB 13 srvtstmqkrayfgxqwpdvdrasvvivhflclapfnfkwa--lrfglvlfaltt 70
OY 125 LGITLCFHRCLTHGCFKLPKLVFFAYCGSLALOGDPMEWVSNHRYHOFVTERDVHS 184
DB 71 lsitfsftrnlshtsrisklpkwywavsavfalqgdpmdwslhrfthqfidsdrphs 130
OY 185 PLOGFWFCHIGVLDKDLFEKRGRRNVNDLKKOAFYRFLOKTYMTHOLALIALLYV 244
DB 131 pkegllfshllwifdtykykcggrdnvidlkkqwyfklitrliaavhllmfwtclily 189
OY 245 GGFPIYVGMGFRVLFVMEHSTFAINSVCHKMGGRPMNTGDLSTNNMFVALCAFGEGWHNN 304
DB 190 gglpylrcggvgfyfigyhtvlnsachlwsrwnlcktsrvnwwlslftmgswnhn 249
OY 305 HHAFQSAARHGLEMWQIDVTWVITLQALIGLATNVKLPTEAKOKL 351
DB 250 hnatessarqglewqjdltwylirllfevlglatvklipseiqkqkm 296

Search completed: September 13, 2002, 09:48:35
Job time: 3764 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM proteIn - protein search, using sw model

Run on: September 13, 2002, 08:47:00 ; Search time 24.84 seconds
(without alignments)
350.061 Million cell updates/sec

Title: US-09-664-840-2

Perfect score: 1946

Sequence: 1 LRSLYFPISISLSLEAM.....ATNWKLPTEAKOKLKAKSA 356

Scoring table:

BLOSUM62
Gapop 10.0, Capext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	650	33.4	1	US-08-309-182B-3
2	555	28.6	2	US-08-663-082-4
3	349.5	18.0	3	US-08-558-823-19
4	326	16.8	1	US-08-742-273-2
5	323.5	16.6	2	US-08-558-823-4
6	273.5	14.1	182	US-08-558-823-5
7	178	9.1	65	US-08-663-082-2
8	111.5	5.7	378	US-08-244-205-7
9	111.5	5.7	378	PCT-US92-10284-7
10	111.5	5.7	404	US-08-244-205-9
11	111.5	5.7	404	PCT-US92-10284-9
12	108.5	5.6	446	US-08-244-205-5
13	108.5	5.6	446	US-09-161-994A-5
14	108.5	5.6	446	PCT-US92-10284-5
15	108.5	5.4	446	PCT-US94-01321-10
16	104.5	5.4	402	US-09-025-578-2
17	101.5	5.2	329	US-09-161-994A-6
18	101.5	5.2	329	US-09-161-994A-9
19	99	5.1	447	US-09-161-994A-7
20	98.5	5.1	447	US-09-161-994A-8
21	95.5	4.9	435	PCT-US94-01321-12
22	94.5	4.9	435	US-08-689-974-5
23	94.5	4.8	460	US-09-058-376-5
24	94	4.8	383	PCT-US94-01321-2
25	92.5	4.8	1865	US-08-588-985-2
26	92.5	4.8	1865	US-08-971-988-2
27	90	4.6	377	US-09-161-994A-12

28	90	4.6	453	2	US-08-244-205-13	Sequence 13, Appl
29	90	4.6	453	4	US-09-161-994A-10	Sequence 10, Appl
30	90	4.6	453	5	PCT-US92-10284-13	Sequence 13, Appl
31	85	4.4	365	2	US-08-833-610-7	Sequence 7, Appl
32	85	4.4	365	3	US-08-834-033A-17	Sequence 17, Appl
33	84	4.3	213	4	US-09-107-383-14	Sequence 14, Appl
34	84	4.3	386	2	US-08-244-205-2	Sequence 2, Appl
35	84	4.3	386	4	US-09-161-994A-11	Sequence 11, Appl
36	84	4.3	386	5	PCT-US92-10284-5	Sequence 5, Appl
37	82.5	4.2	1455	3	US-08-840-062-5	Sequence 156, App
38	81	4.2	316	4	US-08-961-083-156	Sequence 160, App
39	79	4.1	641	4	US-08-961-083-160	Sequence 16, Appl
40	78.5	4.0	383	4	US-09-059-769-12	Sequence 2, Appl
41	78.5	4.0	383	4	US-09-161-994A-16	Sequence 2, Appl
42	78.5	4.0	461	2	US-08-672-814D-2	Sequence 2, Appl
43	78.5	4.0	461	2	US-09-333-696-2	Sequence 2, Appl
44	78	4.0	1311	2	US-08-540-406-4	Sequence 4, Appl
45	78	4.0	1311	3	US-08-656-055-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-309-182B-3
; Sequence 3, Application US/08309182B
; Patent No. 5639645
GENERAL INFORMATION:
; APPLICANT: NO. 563964510 MURATA
; TITLE OF INVENTION: A RECOMBINANT 9 DESATURASE AND A GENE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESS: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/309 182B
; FILING DATE: September 20, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 318 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-309-182B-3

Query Match 33.4%; Score 650; DB 1; Length 318;
Best Local Similarity 45.5%; Pred. No. 3.7e-64;
Matches 116; Conservative 48; Mismatches 87; Indels 4; Gaps 2;

SYNOPSIS: KZ DEC
 75-08-663-082-4

Best Local Similarity 20.3%; Pred. no. 1.3e 20;
Matches 93; Conservative 70; Mismatches 146; Indels 45; Gaps 1

Query match 16.88; Score 326; DB 1; Length 510;

```

Query Match      16.6%; Score 323.5; DB 2; Length 349;
Best Local Similarity 31.7%; Pred. No. 1e-27;
Matches 80; Conservative 37; Mismatches 102; Indels 33; Gaps 8
QY 80 KMNPRDIO-----NATVLVLVLAALAMAFYPS-----WDAFWISFILLGASCVLGTTC 130
  |  | : | : | | | | : | : : | | |

```

Db 28 KTTPRKYITVNTLFTSYAH-LAALYGLYLSFTSAKWTLLTFEVL--FHMSNIGTAG 84
 QY 131 FRRCLTHGGFKLPKLYEFAFCGSLAQGDPMWVSNRRYHQFVDERVHSTQGF 190
 Db 85 ARLMTHTKFAKLPLEIYLMIFNSLAFONTAITWAREHRLHHKSDTDADPHNARSQF 144
 QY 191 FCHIGWLDKDLFEKRGGRNNVNDLKKQAFYRFLOKTYMHOL-----ALIALLYVGG 245
 Db 145 YSHVGMVLVKKHPDLKTKGTDMSDVYNNPYLKF-QKKYAVPLIGYCFALPTLI----- 199
 QY 246 GPPIYWGNG-----FRLVFMHSTFAINSYCHKRGGRPNWTDGLSTNNMVALCA 296
 Db 200 --PYCWMGSMNNAMHIALFRITFPLNTFVLSAHHWGNKPYDKSLIPQNLVSELA 257
 QY 297 FEGGWHNNHAF 308
 Db 258 SGEGFHNHAF 269

RESULT 6

US-08-558-823-5
 ; Sequence 5, Application US/08558823
 ; Patent No. 5876994
 ; GENERAL INFORMATION:
 ; APPLICANT: Knipple, Douglas C.
 ; APPLICANT: Roelofs, Wendell L.
 ; APPLICANT: Miller, Stuart J.
 ; TITLE OF INVENTION: PHEROMONE DESATURASES
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
 ; STREET: Clinton Square, P.O. Box 1051
 ; CITY: Rochester
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 14603
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentln Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/558,823
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Rogalsky Esq., Peter
 ; REGISTRATION NUMBER: 38,601
 ; REFERENCE/DOCKET NUMBER: 19603/400
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (716) 263-1634
 ; TELEFAX: (716) 263-1600
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 182 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-558-823-5

Query Match 14.1%; Score 273.5; DB 2; Length 182;
 Best Local Similarity 31.7%; Pred. No. 1.5e-22;
 Matches 60; Conservative 31; Mismatches 77; Indels 21; Gaps 4;

QY 132 HRCITHGCFKLPKLYEFAFCGSLAQGDPMWVSNRRYHQFVDERVHSTQGF 191
 Db 1 HRLMSHTKFAKLPLEIYLMIFNSLAFONTAITWAREHRLHHKSDTDADPHNARSQF 60
 QY 192 CHIGWLDKDLFEKRGGRNNVNDLKKQAFYRFLOKTYMHOL-----ALIALLYVGG 246
 Db 61 SHVGMVLVKKHPDLKTKGTDMSDVYNNPYLKF-QKKYAVPLIGYCFALPTLI----- 114

QY 247 FPIYWGNG-----FRLVFMHSTFAINSYCHKRGGRPNWTDGLSTNNMVALCA 297
 Db 115 -PYCWMGSMNNAMHIALFRITFPLNTFVLSAHHWGNKPYDKSLIPQNLVSELA 173
 QY 298 GEGWHNNH 306
 Db 174 GEGFHNH 182

RESULT 7

US-08-663-082-2
 ; Sequence 2, Application US/08663082
 ; Patent No. 6043411
 ; GENERAL INFORMATION:
 ; APPLICANT: NISHIZAWA, Osamu
 ; APPLICANT: TOGURI, Toshihiro
 ; TITLE OF INVENTION: GENE FOR FATTY ACID DESATURASE, VECTOR
 ; TITLE OF INVENTION: CONTAINING SAID GENE, PLANT TRANSFORMED WITH SAID GENE,
 ; AND PROCESS FOR CREATING SAID PLANT
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentln Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/663,082
 ; FILING DATE: 25-JUN-1996
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/JP94/02288
 ; FILING DATE: 28-DEC-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 93/352858
 ; FILING DATE: 28-DEC-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BENT, Stephen A.
 ; REGISTRATION NUMBER: 29,768
 ; REFERENCE/DOCKET NUMBER: 81356/107
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202)672-5300
 ; TELEFAX: (202)672-5399
 ; TELEX: 904136
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 65 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; ORIGINAL SOURCE:
 ; ORGANISM: Anabaena variabilis
 ; STRAIN: IAM M-3
 ; US-08-663-082-2

Query Match 9.1%; Score 178; DB 3; Length 65;
 Best Local Similarity 49.2%; Pred. No. 1.5e-12;
 Matches 32; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

QY 236 ALIALLYYGGPPIYWGNGFRLVFMHSTFAINSYCHKRGGRPNWTDGLSTNNMVALC 295
 Db 1 ALGLLLILGGMSFYWGVPFRLVWYHCTWLVNSGTHKFGRTYDADGRSTNCWMAVL 60
 QY 296 AFEGG 300
 Db 111

Db 61 VFC6G 65

```

RESULT 8
US-08-244-205-7
; Sequence 7, Application US/08244205
; Patent No. 5952544
; GENERAL INFORMATION:
; APPLICANT: Browne, John, Kinney, Anthony J.,
; APPLICANT: Pierce, John, Wierzbicki, Anna M.,
; APPLICANT: Yadev, Narendra S., Perez-Grau, Luis
; TITLE OF INVENTION: Fatty Acid Desaturase Genes
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/244,205
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/804,259
; FILING DATE: 4 DECEMBER 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Floyd, Linda A.
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1036-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-244-205-7

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Query Match 5.7%; Score 111.5; DB 2; Length 378;

Best Local Similarity 23.6%; Pred. No. 0.00047;

Matches 83; Conservative 44; Mismatches 98; Indels 127; Gaps 27;

```

QY 43 PTPPEKTE-----TPKPKDLERFTSEVLERKS--KGFWRKRNPRDIONAVT--LL 93
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 10 PEEEPKTOREFDPGAPP-----FNLAADI--RAAIPIKHCWK--NPKKMSYVRELA 58
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 94 VHALAAMAPF---YFSMDAFWISFLLGPGASVGLITLCFHRCLTHGCF---KLPLV 146
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 59 IYFALAGAAVYLNMLVPLWIAOGTFWMALEVLG-----HDC-GHGSFSDNPLNSV 112
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 147 EYFPAVCSLALOGDPMEMVSNHRYHQ---FVDTEDVH-----SPTOGFWEC 192
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 113 GHLLHSSILVRYHG---WRISHRTHQNHGHVENDESMHPSSEKITYKSLDKPTFRFRFT 168
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 193 -----HIGWVL-----DKDLFEVKRGGRNNVNDLKKOAFYRFLQKTYM 232
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 169 LPLVNLAVPFLYLMARSPGKSGSHYHPDSDLPLPK---ERNDV-----LSTACW 214
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 233 HOLA-LIALLYVVG-----FPY---IWMGGRFLVEMHSTFAINSVCHK----- 274
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 215 TMAAVLVCLNLFVMPGMOLKLYVIRPYWTNWM-LDF-VTILHHHG-----HEDKLPW 265
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

QY 275 WGRPMN--TGDLST-----NNMFVALCARGECGHHNHHAFEGSARGCL 316
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 266 YRKEMSYLRGGLTTLDROYGLINHHDI-----GTHVTHHLEPOTIPHYHL 312
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 9
PCT-US92-10284-7
; Sequence 7, Application PC/TUS9210284
; GENERAL INFORMATION:
; APPLICANT: Browne, John, Kinney, Anthony J.,
; APPLICANT: Pierce, John, Wierzbicki, Anna M.,
; APPLICANT: Yadev, Narendra S., Perez-Grau, Luis
; TITLE OF INVENTION: Fatty Acid Desaturase Genes
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10284
; FILING DATE: 19921203
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/804,259
; FILING DATE: 4 DECEMBER 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Floyd, Linda A.
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1036-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US92-10284-7

```

Query Match 5.7%; Score 111.5; DB 5; Length 378;

Best Local Similarity 23.6%; Pred. No. 0.00047;

Matches 83; Conservative 44; Mismatches 98; Indels 127; Gaps 27;

```

QY 43 PTPPEKTE-----TPKPKDLERFTSEVLERKS--KGFWRKRNPRDIONAVT--LL 93
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 10 PEEEPKTOREFDPGAPP-----FNLAADI--RAAIPIKHCWK--NPKKMSYVRELA 58
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 94 VHALAAMAPF---YFSMDAFWISFLLGPGASVGLITLCFHRCLTHGCF---KLPLV 146
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 59 IYFALAGAAVYLNMLVPLWIAOGTFWMALEVLG-----HDC-GHGSFSDNPLNSV 112
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 147 EYFPAVCSLALOGDPMEMVSNHRYHQ---FVDTEDVH-----SPTOGFWEC 192
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 113 GHLLHSSILVRYHG---WRISHRTHQNHGHVENDESMHPSSEKITYKSLDKPTFRFRFT 168
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 193 -----HIGWVL-----DKDLFEVKRGGRNNVNDLKKOAFYRFLQKTYM 232
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 169 LPLVNLAVPFLYLMARSPGKSGSHYHPDSDLPLPK---ERNDV-----LSTACW 214
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 233 HOLA-LIALLYVVG-----FPY---IWMGGRFLVEMHSTFAINSVCHK----- 274
; : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```


OY 193 -----HIGWVL-----DKDLFEVERKGRNNVNDLKKQAFYFLQKTYWY 232
 Db 195 LPLVLMALPYPLMARSPEGKSGHYHPSDLFLPK-----ERNDV-----LTSACW 240
 OY 233 HOLA-LIALLVYVG-----FPY-----IWMGGRFLVEMFSTPAINSVCHK----- 274
 Db 241 TMAVAVLVCLNFMVGMQMLKLYLRYWYNVM-LDF-VTYLHHNG-----HEDKLPW 291
 OY 275 MGRPMN--TGDLST-----NMFEVALCAFEGGNNHNAFEQSARHGL 316
 Db 292 YMKKESWYLRGGTLTLDNDYGLINNHHDI-----GTHVHHLEPQLPHYHL 338

RESULT 12

US-08-244-205-5
 ; Sequence 5, Application US/08244205
 ; Patent No. 5952544
 ; GENERAL INFORMATION:
 ; APPLICANT: Browae, John, Kinney, Anthony J.,
 ; APPLICANT: Pierce, John, Wierzbicki, Anna M.,
 ; APPLICANT: Yadev, Narendra S., Perez-Grau, Luis
 ; TITLE OF INVENTION: Fatty Acid Desaturase Genes
 ; TITLE OF INVENTION: from Plants
 ; NUMBER OF SEQUENCES: 32
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: E. I. du Pont de Nemours and Company
 ; STREET: 1007 Market Street
 ; CITY: Wilmington
 ; STATE: Delaware
 ; COUNTRY: U.S.A.
 ; ZIP: 19898
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Macintosh
 ; OPERATING SYSTEM: Macintosh System, 6.0
 ; SOFTWARE: Microsoft Word, 4.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/244, 205
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/804,259
 ; FILING DATE: 4 DECEMBER 1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Floyd, Linda A.
 ; REGISTRATION NUMBER: 33,692
 ; REFERENCE/DOCKET NUMBER: BB-1036-A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (302) 992-4929
 ; TELEFAX: (302) 892-7949
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 446 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-244-205-5

Query Match 5.6%; Score 108.5; DB 2; Length 446;
 Best Local Similarity 22.0%; Pred. No. 0.0013;
 Matches 89; Conservative 47; Mismatches 121; Indels 147; Gaps 28;

OY 1 LRLSLYFPISISLSLEMAASF-----IATTP-AMPAFASVLDPKIPKPEPKTEPK 54
 Db 36 LSSSSKTSSTSSPLSGFNSRDGFTRNKALNVSTPLTPIF-----EESPL 80
 OY 55 PKDLERFRTSEV-----VLEKSKGFV-RRKWP-----RDIONAVTLVLAALAM 101
 Db 81 EEDNKRQRPDGPAPPPFNADIRAAIPKHCWKNPKMSLSYVVDV-----AIVFALAAG 134
 OY 102 APF-----YESMDAFWISFILLGFASGVIGITLCFHRCLTHGFG-----KLPKLYVEFFAYCG 154

Db 135 AAYLNNTIWEPLVLAOGTFEMALFVLG-----HDC-GHGSFSDNPKLNSVGHLLHSSI 188
 OY 155 SLALQDPMEMVSNHRYNHQ-----FVDERDVH-----SPQGFWFC----- 192
 Db 189 LVPYHG-----WRISHRTHQNHGHVENDESMHPMSKITYTLDKPRFRFTPLPLVLAAY 244
 OY 193 -HIGWVL-----DKDLFEVERKGRNNVNDLKKQAFYFLQKTYWYHOLA--LI 238
 Db 245 PFLVLMARSPGKSGHYHPSDLFLPK-----ERKDV-----LTSACWTAMAAALLY 290
 OY 239 ALLYYVG-----GPPY-----IWMGGRFLVEMFSTPAINSVCHK-----WGRPMN- 281
 Db 291 CLNFTTGPIMKLYGIPRYINVM-LDF-VTYLHHNG-----HEDKLPWYRKESWY 341
 OY 282 -TGDLST-----NMFEVALCAFEGGNNHNAFEQSARHGL 316
 Db 342 LRGLTTLTLDNDYGLINNHHDI-----GTHVHHLEPQLPHYHL 380

RESULT 13

US-09-161-994A-5
 ; Sequence 5, Application US/09161994A
 ; Patent No. 6333448
 ; GENERAL INFORMATION:
 ; APPLICANT: BAFOR, Maureen
 ; APPLICANT: BANAS, Antoni
 ; APPLICANT: DAHLQVIST, Anders
 ; APPLICANT: GUMMELSON, Per-Olov
 ; APPLICANT: LEE, Michael
 ; APPLICANT: SJODAL, Stefan
 ; APPLICANT: STYMANE, Sten
 ; APPLICANT: LENMAN, Marit
 ; TITLE OF INVENTION: NOVEL PLANT ENZYME AND USE THEREOF
 ; FILE REFERENCE: BAFOR-1
 ; CURRENT APPLICATION NUMBER: US/09/161,994A
 ; PRIOR FILING DATE: 1998-09-29
 ; PRIOR APPLICATION NUMBER: 9601236.4
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 446
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; US-09-161-994A-5

Query Match 5.6%; Score 108.5; DB 4; Length 446;
 Best Local Similarity 22.0%; Pred. No. 0.0013;
 Matches 89; Conservative 47; Mismatches 121; Indels 147; Gaps 28;

OY 1 LRLSLYFPISISLSLEMAASF-----IATTP-AMPAFASVLDPKIPKPEPKTEPK 54
 Db 36 LSSSSKTSSTSSPLSGFNSRDGFTRNKALNVSTPLTPIF-----EESPL 80
 OY 55 PKDLERFRTSEV-----VLEKSKGFV-RRKWP-----RDIONAVTLVLAALAM 101
 Db 81 EEDNKRQRPDGPAPPPFNADIRAAIPKHCWKNPKMSLSYVVDV-----AIVFALAAG 134
 OY 102 APF-----YESMDAFWISFILLGFASGVIGITLCFHRCLTHGFG-----KLPKLYVEFFAYCG 154
 Db 135 AAYLNNTIWEPLVLAOGTFEMALFVLG-----HDC-GHGSFSDNPKLNSVGHLLHSSI 188
 OY 155 SLALQDPMEMVSNHRYNHQ-----FVDERDVH-----SPQGFWFC----- 192
 Db 189 LVPYHG-----WRISHRTHQNHGHVENDESMHPMSKITYTLDKPRFRFTPLPLVLAAY 244
 OY 193 -HIGWVL-----DKDLFEVERKGRNNVNDLKKQAFYFLQKTYWYHOLA--LI 238
 Db 245 PFLVLMARSPGKSGHYHPSDLFLPK-----ERKDV-----LTSACWTAMAAALLY 290
 OY 239 ALLYYVG-----GPPY-----IWMGGRFLVEMFSTPAINSVCHK-----WGRPMN- 281

Db 291 CLNFTTGPLOMLKLYGIPYINWVM-LDF-VTYLHHHG-----HBDKLPWYRGKEMSY 341

QY 282 -TGDLST-----NNMFVALCARGEGWNNHNAFEQASARHGL 316

Db 342 LRGLTTLTDYGLINNIHNDI-----GTHVHHLFPOLIPHYHL 380

RESULT 14
PCT-US92-10284-5

; Sequence 5, Application PC/TUS9210284
; GENERAL INFORMATION:
; APPLICANT: Browne, John, Kinney, Anthony J.,
; APPLICANT: Pierce, John, Wierzbicki, Anna M.,
; APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
; TITLE OF INVENTION: Fatty Acid Desaturase Genes
; TITLE OF INVENTION: Itom Plants
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10284
; FILING DATE: 19921203
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/804,259
; FILING DATE: 4 DECEMBER 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Floyd, Linda A.
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1036-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 446 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US92-10284-5

Query Match 5.6%; Score 108.5; DB 5; Length 446;
Best Local Similarity 22.0%; Pred. No. 0.0013;
Matches 89; Conservative 47; Mismatches 121; Indels 147; Gaps 28;

QY 1 LRSLYFPISLSLSLEMAASF-----IATTP-AMPAFASVLDPKIPKPEKTEPK 54

Db 36 LSSSYKTSSPLSFGINSRSGFTRNNALNVSTPLTPIF-----EESPL 80

QY 55 PKDLERFRTSEV-----VLERKSKGFV-RRKNP-----RDIQNAVTLVLHAIAM 101

Db 81 EEDKNQRPFGAPPFNADIRAIIPKHCWKPKMSLSYVVRDY-----AIFALAAAG 134

QY 102 APF---YFSWDAFWISFILLGFASGVLTITCFHRCLHNGF---KLPKLYEFPAYCG 154

Db 135 AAYLNMMIYWPPLYWLAOGTFMFAFLVIG---HDC-GHGSFSDPKLSNVYGHLLHSSI 188

QY 155 SLALQDPMEMVSNHRYHNO---FVDTEDVH-----SPTQGFWFC-----192

Db 189 LVPYHG---WRISHRTHQNHGHVENDSWHPMSEKITYNTLDKPTREFRFTLPLVMILAY 244

QY 193 -HIGWVL-----DKDLFEVKRGRNNVNDLKKQAFYRFLQKTYMHOLA--LI 238

Db 245 PFLYMARSPGKSGSHYHPDSLFLPK---ERKDV-----LSTACTAMAAALV 290

QY 239 ALLXYVG-----GFPY---IYMGGRFLVEMFSTPAINSVCHK---WGSRPN- 281

Db 291 CLNFTTGPLOMLKLYGIPYINWVM-LDF-VTYLHHHG-----HBDKLPWYRGKEMSY 341

QY 282 -TGDLST-----NNMFVALCARGEGWNNHNAFEQASARHGL 316

Db 342 LRGLTTLTDYGLINNIHNDI-----GTHVHHLFPOLIPHYHL 380

RESULT 15
PCT-US94-01321-10

; Sequence 10, Application PC/TUS9401321
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Altered linoleic and linoleic Acid Content
; NUMBER OF SEQUENCES: 72
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01321
; FILING DATE: 04-FEB-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/156551
; FILING DATE: 22-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/014431
; FILING DATE: 05-FEB-1993
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 446 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-01321-10

Query Match 5.6%; Score 108.5; DB 5; Length 446;
Best Local Similarity 22.0%; Pred. No. 0.0013;
Matches 89; Conservative 47; Mismatches 121; Indels 147; Gaps 28;

QY 1 LRSLYFPISLSLSLEMAASF-----IATTP-AMPAFASVLDPKIPKPEKTEPK 54

Db 36 LSSSYKTSSPLSFGINSRSGFTRNNALNVSTPLTPIF-----EESPL 80

QY 55 PKDLERFRTSEV-----VLERKSKGFV-RRKNP-----RDIQNAVTLVLHAIAM 101

Db 81 EEDKNQRPFGAPPFNADIRAIIPKHCWKPKMSLSYVVRDY-----AIFALAAAG 134

QY 102 APF---YFSWDAFWISFILLGFASGVLTITCFHRCLHNGF---KLPKLYEFPAYCG 154

Db 135 AAYLNMMIYWPPLYWLAOGTFMFAFLVIG---HDC-GHGSFSDPKLSNVYGHLLHSSI 188

QY 155 SLALQDPMEMVSNHRYHNO---FVDTEDVH-----SPTQGFWFC-----192

Db 189 LVPYHG---WRISHRTHQNHGHVENDSWHPMSEKITYNTLDKPTREFRFTLPLVMILAY 244

QY 193 -HIGWVL-----DKDLFEVKRGRNNVNDLKKQAFYRFLQKTYMHOLA--LI 238

Db 245 PFLYMARSPGKSGSHYHPDSLFLPK---ERKDV-----LSTACTAMAAALV 290

QY 239 ALLXYVG-----GFPY---IYMGGRFLVEMFSTPAINSVCHK---WGSRPN- 281

Db 291 CLNFTTGPLOMLKLYGIPYINWVM-LDF-VTYLHHHG-----HBDKLPWYRGKEMSY 341

Fri Sep 13 15:31:16 2002

us-09-664-840-2.rai

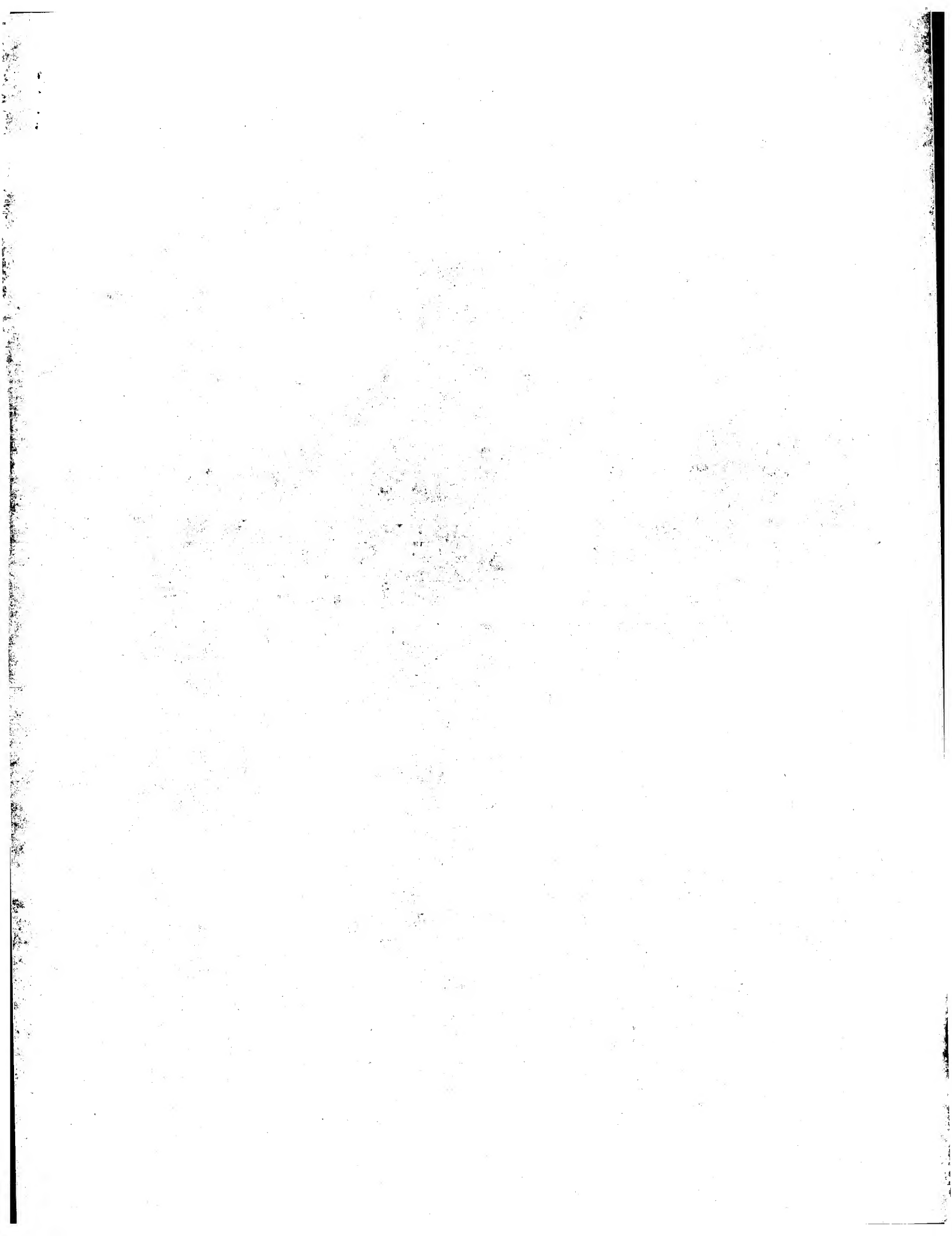
Page 9

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OY 282 -TGDIS-----NMFEVACAFEGEGMNNHHAFFQSARKGL 316
      |::|      ||:      | | | | |
Db 342 LRGGLTLDRDYLGINNNHNDI-----GTHVHTHLEFPQIRPHNL 380

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Search completed: September 13, 2002, 09:49:22
Job time: 3742 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 13, 2002, 08:51:00 ; Search time 43.85 seconds
(without alignments)
780.110 Million cell updates/sec

Title: US-09-664-840-2
Sequence: 1 LRSLVFPSTLSLSLEAM.....ATNNVLPTEAKOKIKAKSA 356
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	887.5	45.6	305	2	T52111
2	874.5	44.9	307	2	T52109
3	870.5	44.7	311	2	G84719
4	833	42.8	299	2	G86196
5	801	41.2	297	1	G61359
6	788.5	40.5	319	2	G86199
7	786.5	40.4	299	2	G86199
8	775.5	39.9	299	2	B86196
9	741	38.1	287	2	E86196
10	687	35.3	272	2	A17005
11	650	33.4	318	1	S75765
12	567.5	29.2	285	1	AG2429
13	556	28.6	278	1	S57643
14	423.5	21.8	479	2	T40925
15	402	20.7	493	2	S71634
16	359	18.4	451	1	UC6180
17	358.5	18.4	439	2	T28019
18	352	18.1	486	2	T18228
19	349.5	18.0	358	1	A24699
20	349	17.9	355	2	A32115
21	347.5	17.9	338	2	T287823
22	342.5	17.6	345	2	PC7092
23	338	17.4	476	2	S52746
24	329.5	16.9	333	2	T26230
25	329.5	16.9	358	1	A36507
26	326	16.8	510	1	S64059
27	324	16.6	397	2	F97707
28	319	16.4	395	2	F71711
29	215.5	11.1	237	2	I54779

30	206	10.6	392	2	F83610	Probable fatty ac
31	114	5.9	359	2	S52650	omega-3 fatty acid
32	111.5	5.7	404	2	Q08612	omega-3 fatty acid
33	108.5	5.6	446	1	JQ2336	omega-3 fatty acid
34	108.5	5.6	447	1	T43319	Deltas fatty acid
35	105	5.4	380	2	T10898	Probable omega-3 f
36	103	5.3	454	2	H88791	protein T13P2.1 (l
37	102	5.2	377	2	B83454	probable alkane hy
38	101.5	5.2	359	2	AG2005	omega-3 fatty acid
39	99.5	5.1	380	2	T06235	omega-3 fatty acid
40	99	5.1	460	2	T10063	omega-3 fatty acid
41	99	5.1	537	2	T51785	omega-3 fatty acid
42	98.5	5.1	438	2	T15039	omega-3 fatty acid
43	95	4.9	514	2	B64634	omega-3 fatty acid
44	94	4.8	383	1	A44227	omega-3 fatty acid
45	93.5	4.8	398	2	T01696	omega-3 fatty acid

ALIGNMENTS

RESULT 1
T52111
stearoyl-CoA desaturase (EC 1.14.99.5) ADS1 [imported] - Arabidopsis thaliana
N:Alternate names: delta 9 desaturase ADS1
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 31-Mar-2001
R:Fukuchi-Mizutani, M.; Tasaka, Y.; Tanaka, Y.; Ashikari, T.; Kusumi, T.; Murata, N.
Plant Cell Physiol. 39, 247-253, 1998
A:Title: Characterization of delta9 acyl-11lipid desaturase homologues from Arabidopsis
A:Reference number: 225959
A:Accession: T52111
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-305 <FUK>
A:Cross-References: EMBL:D88536; PDB:BAA25180.1
C:Genetics:
A:Gene: ADS1
C:Superfamily: mammalian stearoyl-CoA desaturase; stearoyl-CoA desaturase homology
C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 45.6%; Score 887.5; DB 2; Length 305;
Best Local Similarity 51.4%; Pred. No. 4.2e-72;
Matches 152; Conservative 53; Mismatches 88; Indels 3; Gaps 2;
QY 56 KDDLRFRFSEVYLERKSKGFRRKRNPRDIONAVTLVLHALLAMAPFYFSWDAFWISF 115
DB 9 EENNKKMADAKEMGRKRAMERKRLDIYKAPASLFEVHFLCLADPFNFTWPAALVAL 68
QY 116 ILGFAAGVLTGTLTGFHRCITLHGFELPKLVEYFPAYGSLAGDDEPMENSRINHOE 175
DB 69 IV--YTVGGLGTVSYHNHLNLRSKFKPKLWLEFFAYCGLATIGDDPIDWSTJRHVHOE 126
QY 176 VDEEDVHSPPOGFWECHIGVLDKDLFEKRGGRNNVNDLAKOAFRFLOKTYMYHOE 235
DB 127 TDSDDPHSPNEGFEWFSHLMLEFDGYLER--CGRRTVEDLKLQMYKFLQRYVLHIL 185
QY 236 ALIALLYVGGPRVYVMGMRFLVPMHSTPAISVCKKMGGRWNGDLSSTNNFVALC 295
DB 186 TFGFLLYTFGGISFTVMGSLGVAMEHHVTCILNSLCVWGSRTWKYNDTSRNWMLSVF 245
QY 296 AFEQGMHNNHAFQDSARHGLEMMQIDVTYVITLQIGLATVVKLPTEAKOKKL 351
DB 246 SEGESWNNHHAFFSSARQGLEMMQIDISWIVAFLEIGLATVVKLPESQRNRH 301
RESULT 2
T52109
stearoyl-CoA desaturase (EC 1.14.99.5) [imported] - Arabidopsis thaliana
N:Alternate names: delta 9 desaturase
C:Species: Arabidopsis thaliana (mouse-ear cress)

[illegible][illegible]

OY 319 WQIDVTVVIRTLQAIIGLATNVKLPTEAO 347
 DB 244 WEVDLTWMTVOLQILGLATNVKLPTEAO 272

RESULT 11

S57565
 stearyl-CoA desaturase (EC 1.14.99.5) 1 - *Synechocystis* sp. (strain PCC 6803)
 N:Alternate names: acyl-CoA desaturase 1; delta9 fatty acid desaturase; protein sll0541
 C:Species: *Synechocystis* sp.
 A:Variety: PCC 6803
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimp, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, D. N. Res. 3, 109-136, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp.
 A:Reference number: S74322; MID:97061201
 A:Accession: S57565
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-318 <RAN>
 A:Cross-references: EMBL:D64003; GB:AB001339; NID:91001200; PIDN:BA10500.1; PID:9100125
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C:Genetics:
 A:Gene: des9
 C:Superfamily: mammalian stearyl-CoA desaturase; stearyl-CoA desaturase homology
 C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis
 F:95-278/Domain: stearyl-CoA desaturase homology <SDH>

Query Match 33.4%; Score 650; DB 1; Length 318;
 Best Local Similarity 45.5%; Pred. No. 9.8e-51;

Matches 116; Conservative 48; Mismatches 87; Indels 4; Gaps 2;

OY 91 TLLVLAALMAAPFYSDAFWISFILLGASVGLTLCFHNCLTHGFKLPKLYEYF 150
 DB 61 TSHLVALLAFLRPFSSKAVGNAFLIYITGCT-CITLGFHNCISHRSEFNPWKLEYLF 119
 OY 151 AYCGLALGDDPMWVSNHRYHNOFVDERDVHSPTOGFNCHIGVLDKDFEVRGR 210
 DB 120 VIGCTLACOGGVEWVGLRHMHKFSPTPRPDHNSKGFMSHIGMME--IPAKAI 176
 OY 211 RNVNNDLKAQAFRLQKTYMNLALILALYVGGFPIYVGMGRFLVPMHSTPAINS 270
 DB 177 PRYTKIDIDKRFQFCNNLILIOVALGLILFALGGMFVINGIFRLVFEHFTWVNS 236
 OY 271 VCHKMGSRPMNTGDLSTNNMFVALCAFGEGMNNHNAFQSGARHGLEMMQIDVTWVIRT 330
 DB 237 AFHKFGYVSHESNDYSRNCMMWVALLFLFGGMNNHNAIYOSARHGLQMEVDLWMTIKF 296
 OY 331 LQAIIGLATNVKLPTE 345
 DB 297 LSLGLAKDKLPPE 311

RESULT 12

AG2429
 delta-9 desaturase [Imported] - *Anabaena* sp. (strain PCC 7120)
 C:Species: *Anabaena* sp.
 A:Note: *Anabaena* sp. (strain PCC 7120) is a synonym of *Nostoc* sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
 C:Accession: AG2429
 R:Kaneko, T.; Nakamura, Y.; Maki, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Shimp, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anabaena* sp. strain PCC 7120
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AG2429
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-285 <KUR>
 A:Cross-references: GB:BA000019; PIDN:BA076690.1; PID:917134129; GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: desC
 C:Superfamily: mammalian stearyl-CoA desaturase; stearyl-CoA desaturase homology

Query Match 29.2%; Score 567.5; DB 2; Length 285;
 Best Local Similarity 37.6%; Pred. No. 2.3e-43;

Matches 103; Conservative 58; Mismatches 92; Indels 21; Gaps 5;

OY 78 RRRKNPRDIONAVTLLVLAALMAAPFYSDAFWISFILLGASVGLTLCFHNCLTH 137
 DB 17 RLSTW-----NVAFTTIALALAPFWSWALGL-LFLPMLRSGISICIGYHRLSH 70
 OY 138 GGGKRLKLYEYFPAAGSIALGDDPMWVSNHRYHNOFVDERDVHSPTOGFNCHIGV 196
 DB 71 KSFQVPRKLEVAIVATIGALAMOGGPIFWIGRHONHAHTEVDYLDPRYSQGRFWSHML 130
 OY 197 VL-----DKDLFEVRKGRNNVNDLKAQAFRLQKTYMNLALILALYVGGFPIY 249
 DB 131 ILPRSEFPDYET-----QVAPDLAROPFRMLDRYFILLQIPGLMLYALGWSF 183
 OY 250 IYWGSGFLVFMHSTFALNSVCHKMGSRPMNTGDLSTNNMFVALCAFGEGMNNHNAFE 309
 DB 184 VIYGVVLRVAVLLMHSWTFVNSATHHMGYRTFNADDNARLMMVSIYVYEGCHNNHHTYR 243
 OY 310 QSRHGLEMMQIDVTWVIRTQAIIGLATNVKLP 343
 DB 244 NVAKAGFQWMEVDYTWMSIKLDTGLAKKVL 277

RESULT 13

S57643
 stearyl-CoA desaturase (EC 1.14.99.5) - *Synechococcus* sp.
 N:Alternate names: Delta9 fatty acid desaturase
 C:Species: *Synechococcus* sp.
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jun-2000
 C:Accession: S57643
 R:Nishizawa, O.; Toguri, T.
 submitted to the EMBL Data Library, January 1994
 A:Description: Fatty acid desaturase gene from *Anacystis nidulans*.
 A:Reference number: S57643
 A:Accession: S57643
 A:Molecule type: DNA
 A:Residues: 1-278 <NIS>
 A:Cross-references: EMBL:X77367; NID:9886832; PIDN:CA54556.1; PID:9886833
 A:Note: the source is designated as *Anacystis nidulans*
 C:Superfamily: mammalian stearyl-CoA desaturase; stearyl-CoA desaturase homology
 C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis
 F:54-243/Domain: stearyl-CoA desaturase homology <SDH>

Query Match 28.6%; Score 556; DB 1; Length 278;
 Best Local Similarity 40.1%; Pred. No. 2.4e-42;

Matches 108; Conservative 52; Mismatches 83; Indels 26; Gaps 6;

OY 89 AVTLVLVLAALMAAPFYSDAFWISFILLGASVGLTLCFHNCLTHGFKLPKLY 146
 DB 16 ALFVVAIIGLALLFLRPNFNPVAVG-VVALYITTCGCTGLMHLISIRSEVEPKWL 74
 OY 147 EYFPAAGSIALGDDPMWVSNHRYHNOFVDERDVHSPTOGFNCHIGV-----D 199
 DB 75 EYVLFVCGTGLMNGRIEMWIGLHNRHNLHSDVDHNSKGLFMSHFLMAYITPAKTE 134
 OY 200 KDLFEVRKGRNNVNDLKAQAFRLQKTYMNLALILALYVGGFPIYVGMGRFLVPMH 253
 DB 135 VDKF-----TRIDAGDPVYRFNKKYFFGVQVLLGLVLAWGBAWGNGMSFVWG 184
 OY 254 MGRFLVFMHSTFALNSVCHKMGSRPMNTGDLSTNNMFVALCAFGEGMNNHNAFQSGAR 313
 DB 185 IFARLVVVYVHTVLYNSATIKFGYRSHESGDSITNCMMWVALLFLFGGMNNHNAIYOSAR 244

OY 314 HGLEWQIDVTWYVIRTLQALGATNKL 342
 DB 245 HGLQWMEFDLWLIICGLKKVGLARKIKV 273

RESULT 14

T40925
 stearyl-CoA desaturase (EC 1.14.99.5) SPCC1281.06c [similarity] - fission yeast (Schl

C;Species: Schizosaccharomyces pombe

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Jun-2000

C;Accession: T40925

R;Volckert, G.; Wood, V.; Rajandream, M.A.; Barrell, B.G.

submitted to the EMBL Data Library, January 1999

A;Reference number: Z21957

A;Accession: T40925

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-479 <VOL>

A;Cross-references: EMBL:AL035218; PIDN:CAA22827.1; GSPDB:GN00068; SPDB:SPCC1281.06c

A;Experimental source: Strain 972h-; cosmid c1281

C;Genetics:

A;Gene: SPDB:SPCC1281.06c

A;Map position: 3

C;Superfamily: yeast stearyl-CoA desaturase; cytochrome b5 core homology; stearyl-CoA

C;Keywords: heme; iron; metalloprotein; oxidoreductase

F;104-294/Domain: stearyl-CoA desaturase homology <SDH>

F;390,416/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 21.8%; Score 423.5; DB 2; Length 479;

Best local similarity 30.4%; Pred. No. 3.6e-30;

Matches 106; Conservative 62; Mismatches 142; Indels 39; Gaps 10;

OY 19 AMASTATTTPAMPAPASVLD--PKIPKPEPKTEPRKPDLEFRFRTSEVVLERRSKG 75
 DB 6 AATFASATQPTTEGNASMRKRTIPVPSPERKWDPRKHIOQPMWQ-----N 57
 OY 76 FRRR-KMNPFRDIONAVTLVLVHALAAMAFYFSDAFWISFLLGFASGVLTITCFHRC 134
 DB 58 WNRHLNW-----LRCHLIRGLPMIAIYGVFTTPILOTKILIFAIYYAASGLITGYNHL 112
 OY 135 LTHGFKLPRKLYEYFFAYGSLAOGDPMEVSNHRYHHQVDEVDVHSPQGFCHT 194
 DB 113 WSHRAVKAKKPLEYFLAAGCAAFEGSIRWMSRDRHNRHYDTDKDPYNAKGFYAHV 172
 OY 195 GNVLDKDLFEVRRGGRNNVNDLKKQAEYRFLQKTYMHQALLILVYVGEPY---I 250
 DB 173 GWNII---ILQNPRIGRSDVSDLSDFVEMNHR---HFLPIASPMFT--FPSIFGCL 223
 OY 251 VWC---MGF-----RLVPMFHSFPAINSVCHKMGGRPMNTGDLSTNNMFVALCAFGEGM 301
 DB 224 LMWDYRGYFYAGVCLVYVHNATFCVNSLAHLIGSQPFDDJNSARNHFTALVTLGEGN 283
 OY 302 HNNHNAFEQSARHGLEWQIDVTWYVIRTLQALGATNKLPTPAOKOK 350
 DB 284 HNYHNAFPDYNRGLRWYEDPTKIFITYASLFGALAYNLNTEPDMEIOK 332

RESULT 15

S71634
 stearyl-CoA desaturase (EC 1.14.99.5) - Cryptococcus curvatus

N;Alternate names: Delta9 fatty acid desaturase

C;Species: Cryptococcus curvatus

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000

C;Accession: S71634

R;Meesters, P.A.E.P.; Eggink, G.

Yeast 12, 723-730, 1996

A;Title: Isolation and characterization of a Delta-9 fatty acid desaturase gene from the

A;Reference number: S71634; MUID:96408765

A;Accession: S71634

A;Molecule type: DNA

A;Residues: 1-493 <ME>

A;Cross-references: EMBL:Y10422; NID:g1783356; PIDN:CAA71449.1; PID:g1783357

A;Experimental source: strain CBS570

C;Genetics:

A;Gene: OLE1

C;Superfamily: yeast stearyl-CoA desaturase; cytochrome b5 core homology; stearyl-CoA

C;Keywords: heme; iron; metalloprotein; oxidoreductase; unsaturated fatty acid biosyn

F;119-308/Domain: stearyl-CoA desaturase homology <SDH>

F;372-448/Domain: cytochrome b5 core homology <CBS>

F;406,432/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 20.7%; Score 402; DB 1; Length 493;

Best local similarity 28.9%; Pred. No. 3.2e-28;

Matches 109; Conservative 60; Mismatches 124; Indels 84; Gaps 12;

OY 9 ISTSLSLDAMASFITTTTPAMPAPASVLDPKIPKPEPKTEPRKPDLEFRFRTSEVVL 68
 DB 1 MSASTATPPTTAPAVANPTPAAASAAA---APAAITKKAETIDES--EIFYVS--- 51
 OY 69 LERKSGFWRKKNPDRDIONAVTLVLVHALAAMAFYFSDAFWISF----- 115
 DB 52 -----QNVVTRFY-ENMTMLPPVTVMSNLQNIOWISFTALTVPAMA 92
 OY 116 -----ILLGFASGVLTITCFHRCILTHGFKLPRKLYEYFFAYGSLAL 158
 DB 93 IYGLCTLELQKRTYIMAIYVYFMFG-LGITAGYHRLAHNRYNASADLYFLALCGAGSV 151
 OY 159 QGDPMENVSNHRYHHQVDEVDVHSPQGFCHIGVLDKDLFEVRRGGR-RNNVNDL 217
 DB 152 QGSIKWMSRGRHNRHTDTRKLDIPYSAHEGFWMAHVGWML-----VPRGKIGVADISDL 206
 OY 218 KQAFYRFLQKTYMHQALLILVYVGEPYIYWGKF-----RLVPMFHS 264
 DB 207 SRNPVVKQOHNNY-----VMLVYLMGLV--PPTLVAGWGDMKGLLPAGAAIRLVFNHS 260
 OY 265 TPAINSVCHKMGGRPMNTGDLSTNNMFVALCAFGEGMNNHNAFEQSARHGLEWQIDVT 324
 DB 261 TFCVNSLAHMLGETPFDKHTPKDHFITALVTVGEGIHNFHQHPMDFRNAIKYQYDPT 320
 OY 325 WYVIRTLQALGATNKL 341
 DB 321 KMFITMKNVGLASHLK 337

Search completed: September 13, 2002, 09:50:27

Job time: 3567 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 13, 2002, 09:49:24 ; Search time 24.91 Seconds

(without alignments)
553,358 Million cell updates/sec

Title: US-09-664-840-2

Perfect score: 1946
Sequence: 1 LRSLVPPISISLSLEAM.....ATNVKLPPEAKOKLAKKSA 356

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	349.5	18.0	358	1 ACOD_RAT	P07308 ratius norv
2	346	17.8	355	1 ACOD_MOUSE	P13516 mus musculu
3	344.5	17.7	359	1 ACOD_SHEEP	O62849 ovis aries
4	343.5	17.7	334	1 ACOD_PIG	O02858 sus scrofa
5	343.5	17.7	359	1 ACOD_BOVIN	O91694 bos taurus
6	342	17.6	354	1 ACOD_MESAU	O64420 mesocricetu
7	331.5	17.0	359	1 ACOD_HUMAN	O00767 homo sapien
8	329.5	16.9	358	1 ACOD_MOUSE	P13011 mus musculu
9	326	16.8	510	1 ACOD_YEAST	P21147 saccharomyc
10	111.5	5.7	404	1 FD3C_BRANA	P48618 brassica na
11	108.5	5.6	446	1 FD3C_ARATH	P46310 arabidopsis
12	105	5.4	380	1 FD3C_PNAU	P32291 phaseolus a
13	99	5.1	460	1 FD3C_RICCO	P48619 ricinus com
14	98.5	5.1	447	1 FD3C_SRSIN	P48620 sesamum ind
15	95.5	4.9	435	1 FD3C_ARATH	P48622 arabidopsis
16	94	4.8	383	1 FD32_BRANA	P48624 brassica na
17	92.5	4.8	759	1 PMT6_YEAST	P42934 saccharomyc
18	91.5	4.7	530	1 MATP_HUMAN	O9umk9 homo sapien
19	90	4.6	377	1 FD31_BRANA	P46311 brassica na
20	90	4.6	453	1 FD3C_SOYBN	P48621 glycine max
21	89.5	4.6	369	1 XYLM_PSEPU	P21395 pseudomonas
22	89	4.6	330	1 RCENK_ERKSP	P26279 erythrobact
23	88.5	4.5	635	1 S6A8_BOVIN	O18875 bos taurus
24	88	4.5	975	1 PMPA_CHLTR	O84417 chlamydia t
25	87.5	4.5	1394	1 CNM4_BOVIN	O28181 bos taurus
26	86	4.4	1411	1 Y297_HUMAN	O15040 homo sapien
27	85.5	4.4	635	1 S6A8_RAT	P28510 rattus norv
28	84	4.3	213	1 AMIS_MYCSM	P56583 mycobacteri
29	84	4.3	386	1 FD3E_ARATH	P48623 arabidopsis
30	83	4.3	389	1 O85C_DROME	O9vnh6 drosophila
31	82	4.2	515	1 TLG1_CHLUP	O92812 chlamydia p
32	81.5	4.2	530	1 MATP_MOUSE	P58335 mus musculu
33	81.5	4.2	635	1 S6A8_HUMAN	P48029 homo sapien

34	80.5	4.1	329	1 COX3_ACACA	O37374 acanthamoeb
35	80.5	4.1	426	1 S6A8_HUMAN	P53796 homo sapien
36	80	4.1	1672	1 PMPA_CHLMD	O9pij2 chlamydia m
37	79.5	4.1	379	1 FD3E_TOBAC	P48626 nicotiana t
38	78.5	4.0	262	1 COX3_ANOQU	P33508 anopheles q
39	78.5	4.0	461	1 CD51_HUMAN	O92903 h phosphati
40	78	4.0	709	1 FZD6_MOUSE	O61089 mus musculu
41	77.5	4.0	327	1 ENF2_MOUSE	O61672 m equilibra
42	77.5	4.0	418	1 EFIG_ORYSA	O9217 oryza sativ
43	77.5	4.0	476	1 MM10_HUMAN	P09238 homo sapien
44	77.5	4.0	909	1 CNM4_HUMAN	O14028 homo sapien
45	77	4.0	410	1 Y588_BUCAL	P57648 buchnera ap

ALIGNMENTS

RESULT 1
ACOD_RAT ID ACOD_RAT STANDARD: PRT: 358 AA.
AC P07308;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Acyl-CoA desaturase (EC 1.14.99.5) (Stearoyl-CoA desaturase) (Fatty acid desaturase) (Delta(9)-desaturase).
GN SCD.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
NC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP MEDLINE=87008535; PubMed=2428815;
RA Thiede M.A., Ozols J., Strittmatter P.;
RT "Construction and sequence of cDNA for rat liver stearyl coenzyme A desaturase.";
RL J. Biol. Chem. 261:13230-13235(1986).
CC -1- FUNCTION: TERMINAL COMPONENT OF THE LIVER MICROSOMAL STEARYL-COA DESATURASE SYSTEM. THAT UTILIZES O(2) AND ELECTRONS FROM REDUCED CYTOCHROME B(5) TO CATALYZE THE INSERTION OF A DOUBLE BOND INTO A SPECTRUM OF FATTY ACYL-COA SUBSTRATES AMONG WHICH PALMITOYL-COA AND STEAROYL-COA.
CC -1- CATALYTIC ACTIVITY: Stearoyl-CoA + AH(2) + O(2) -> oleoyl-CoA + A + 2 H(2)O.
CC -1- COFACTOR: IRON.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic reticulum (Probable).
CC -1- INDUCTION: THIS PROTEIN IS THE ONLY INDUCIBLE COMPONENT OF THIS FATTY ACYL-COA DESATURASE SYSTEM.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- MISCELLANEOUS: DESATURASE HAS A HALF-LIFE OF ONLY 4 HOURS.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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CC -----
CC EMBL: J02585; AAA42116.1; -.
CC PIR: A24699; A24699.
CC InterPro: IPR001522; Desaturase.
CC Pfam: PF01069; Desaturase.1.
CC PRINTS: PR00075; PACDSATPRASE.
CC ProDom: PD002221; Desaturase.1.
CC PROSITE: PS00476; FATTY_ACID_DESATUR_1; 1.
CC OxiReductase; Fatty acid biosynthesis; Transmembrane; Endoplasmic reticulum; Iron.
CC TRANSMEM 75 95 POTENTIAL.


```

DE acid desaturase (Delta(9)-desaturase).
GN SCD.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID:9940;
RN [1]
  SEQUENCE FROM N.A.
  STRAIN-Y1089; TISSUE-Adipose tissue;
  MEDLINE-98223428; PubMed-9554990;
  RA Ward R.J., Travers M.T., Richards S.E., Vernon R.G., Salter A.M.,
  RA Buttery P.J., Barber M.C.;
  RA "Stearoyl-CoA desaturase mRNA is transcribed from a single gene in the
  RT ovine genome.";
  RT Blochlin. Biophys. Acta 1391:145-156(1998).
  CC -1- FUNCTION: TERMINAL COMPONENT OF THE LIVER MICROSOMAL STEAROYL-COA
  CC DESATURASE SYSTEM, THAT UTILIZES O(2) AND ELECTRONS FROM REDUCED
  CC CYTOCHROME B(5) TO CATALYZE THE INSERTION OF A DOUBLE BOND INTO A
  CC SPECTRUM OF FATTY ACYL-COA SUBSTRATES AMONG WHICH PALMITOYL-COA
  CC AND STEAROYL-COA (BY SIMILARITY).
  CC -1- CATALYTIC ACTIVITY: Stearoyl-CoA + AH(2) + O(2) = oleoyl-CoA + A +
  CC 2 H(2)O.
  CC -1- COFACTOR: IRON.
  CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
  CC reticulum (Probable).
  CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
  CC AND/OR BE INVOLVED IN METAL ION BINDING.
  CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
  CC -----
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  CC or send an email to license@isb-sib.ch).
  CC -----
  DR EMBL; AJ001048; CAA04502.1; -.
  DR InterPro: IPR001522; Desaturase.
  DR Pfam: PF01069; Desaturase: 1.
  DR PRINTS: PR00075; PACDSATRASE.
  DR Prodom: PD002221; Desaturase: 1.
  DR PROSITE: PS00476; FATTY_ACID_DESATUR_1; 1.
  KW Oxidoreductase; Fatty acid biosynthesis; Transmembrane;
  KW Endoplasmic reticulum; Iron.
  FT TRANSMEM 76 96 POTENTIAL.
  FT TRANSMEM 98 118 POTENTIAL.
  FT TRANSMEM 223 243 POTENTIAL.
  FT TRANSMEM 315 335 POTENTIAL.
  FT DOMAIN 120 125 HISTIDINE BOX 1.
  FT DOMAIN 157 161 HISTIDINE BOX 2.
  FT DOMAIN 298 302 HISTIDINE BOX 3.
  SQ SEQUENCE 359 AA; 41671 MW; 219CFBDB1E35418 CRC64;

Query Match 17.7%; Score 344.5; DB 1; Length 359;
Best Local Similarity 27.4%; Pred. No. 1,1e-22;
Matches 101; Conservative 56; Mismatches 144; Indels 67; Gaps 11;

15 LSLLEMASFIATTTTPAMPFAVSLD-----PKIP-----TKRPK-----TET 52
DB 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
6 LOBEISSSTTTTITTAPP-SVYLDNNGGKLEKTPLYEEDIRPMRDIDYDPNQDEG 64
QY 53 PRPKDLEFRTESEVLEKRSKGFRRKRNPRDIONAVTLVLAHLA-----AMAFPSW 108
DB 65 PRPK-----LEV-----VVR-----NILLMGLHLAGALXGTLIPTCXIT 99
QY 109 DAFWISFILGFASGVLTITLFCRHCLTHGFKLPKLYEPFANGSIALOGDPNENWSN 168
DB 100 TELWLVLF---YVISALGLTIGVHRLMSHRYKARLPRLVLIANTVAFONDVEFSRD 156
QY 169 HRYHQFVTERDVHSPDQGEFCHIGVLDKDLFVEKRGGRNNVNDLKKQAFYRFLQK 228

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DB 157 HRAHKKFSETDADPHNSRRGFESHGMLVRRHNPVREKATLSDLSRAELVNFQR 216
QY 229 TYMHQALATLALYYVGGFYIWMGMF-----RLVMEHSTPLINSCHWGR 278
DB 217 YKRGVILLCFILPTL--VPWYLMGESFONSLEFATFLKRAYLVNATWLVNSAAHMYGYR 274
QY 279 PWNFGDLSTNNMFVALCAREGHNHNAFEQSARGLEMMQIDVTWYVIRTLQATGLAT 338
DB 275 PYKRTNPRENILVLSGAVGEGFNHHTPEYDSASEYRMHINTFTFDCAAIIGLAY 334
QY 339 NVKLPTFA 346
DB 335 DRKKVSKA 342

RESULT 4
ACOD_PIG STANDARD; PRT; 334 AA.
ID ACOD_PIG 002858;
DT 15-JUL-1998 (rel. 36, Created)
DT 15-JUL-1998 (rel. 40, Last sequence update)
DE 16-OCT-2001 (rel. 40, Last annotation update)
DE Acyl-CoA desaturase (EC 1.14.99.5) (Stearoyl-CoA desaturase) (Fatty
DE acid desaturase) (Delta(9)-desaturase) (Fragment).
GN SCD.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID:9623;
RN [1]
  SEQUENCE FROM N.A.
  Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
  RA Fumagali O.;
  RA -1- FUNCTION: TERMINAL COMPONENT OF THE LIVER MICROSOMAL STEAROYL-COA
  RA DESATURASE SYSTEM, THAT UTILIZES O(2) AND ELECTRONS FROM REDUCED
  RA CYTOCHROME B(5) TO CATALYZE THE INSERTION OF A DOUBLE BOND INTO A
  RA SPECTRUM OF FATTY ACYL-COA SUBSTRATES AMONG WHICH PALMITOYL-COA
  RA AND STEAROYL-COA (BY SIMILARITY).
  RA -1- CATALYTIC ACTIVITY: Stearoyl-CoA + AH(2) + O(2) = oleoyl-CoA + A +
  RA 2 H(2)O.
  RA -1- COFACTOR: IRON.
  RA -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
  RA reticulum (Probable).
  RA -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
  RA AND/OR BE INVOLVED IN METAL ION BINDING.
  RA -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
  RA -----
  RA This SWISS-PROT entry is copyright. It is produced through a collaboration
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  RA use by non-profit institutions as long as its content is in no way
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  RA or send an email to license@isb-sib.ch).
  RA -----
  DR EMBL; Z97186; CAB10004.1; -.
  DR InterPro: IPR001522; Desaturase.
  DR Pfam: PF01069; Desaturase: 1.
  DR Prodom: PD002221; Desaturase: 1.
  DR PROSITE: PS00476; FATTY_ACID_DESATUR_1; 1.
  KW Oxidoreductase; Fatty acid biosynthesis; Transmembrane;
  KW Endoplasmic reticulum; Iron.
  FT TRANSMEM 1 1 POTENTIAL.
  FT TRANSMEM 65 85 POTENTIAL.
  FT TRANSMEM 87 107 POTENTIAL.
  FT TRANSMEM 212 232 POTENTIAL.
  FT TRANSMEM 304 324 POTENTIAL.
  FT DOMAIN 109 114 HISTIDINE BOX 1.
  FT DOMAIN 146 150 HISTIDINE BOX 2.
  FT DOMAIN 287 291 HISTIDINE BOX 3.
  FT NON_TER 334 334
  SQ SEQUENCE 334 AA; 38482 MW; 79183E3918469977 CRC64;

```


Query Match 17.7% Score 343.5; DB 1; Length 334;
 Best Local Similarity 28.3%; Pred. No. 1.2e-22;
 Matches 99; Conservative 64; Mismatches 144; Indels 43; Gaps 13;

21 ASFTATTPPAMPAPASVLD-----DPKIPPKPEPKTPPKPDLD--ERRTSEVLEERK 72
 1 SSVTTTTTTPAS-SRVLONGGKSEKTPPYVEDIR-PEKRDIDYPTODKEGP-OGK 57
 73 SKGWRKRNPRDIONAVTLVLHALLA-----AMAPFFSMDAF-ISEFLLGASVGLI 127
 58 LEYWR-----NIIIMSLHLAGALGILLPTCKIYILLMAFYLL-----SAVG 104
 128 TLCFHRLTHGGFKLPKLYEYFAVCGSLALOGDPMEMVSNHRHYHQFVTERDVSPTQ 187
 105 TAGAHRMSHTYKARLEPLRFELIANTMARQNDYEMARDHRAHNFSETDADPHNSRR 164
 188 GFWRCHIGWVL-DKDLFEYKRGRRNNVNDLKKQAFRELOKTYMQLALILLYVVG 246
 165 GFESHWMLLVKRPVAVKEKGLL-NMSDKAEKLYVFORRYKPGILLMCFILPTI-- 221
 247 FRYIWMGCF-----RLVFEHSTFAINSYCHKWGRPNNTGDLSTNNMFALCA 296
 222 VPMTCWGAEPFOSLFVATFLKAYLATWLVNSAHLXGTRPYDKTISRENILVSLGA 281
 297 FGEGRNNHAFEGSARHGLEWMOIDVTWYVIRLQATGNVAKLPEEA 346
 282 VGEFHNHYHFFPYDYSASEYRMHINTLTFIDCMAALGLAYDRKAKSKA 331

RESULT 5
 ACOD_BOVIN STANDARD; PRT; 359 AA.

AC 09T94;
 16-OCT-2001 (Rel. 40, Created)
 16-OCT-2001 (Rel. 40, Last sequence update)
 16-OCT-2001 (Rel. 40, Last annotation update)
 Acyl-CoA desaturase (EC 1.14.99.5) (Stearoyl-CoA desaturase) (Fatty acid desaturase) (Delta(9)-desaturase).
 SCD.
 Bos taurus (Bovine).
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;
 [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=adipose tissue;
 RC Chung M.I., Ha S.H., Baik M.G., Choi Y.J.;
 RT "Cloning and characterization of full-coding cDNA of bovine stearoyl CoA desaturase from adipose tissue."
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: TERMINAL COMPONENT OF THE LIVER MICROSOMAL STEAROYL-COA DESATURASE SYSTEM, THAT UTILIZES O(2) AND ELECTRONS FROM REDUCED CYTOCHROME B(5) TO CATALYZE THE INSERTION OF A DOUBLE BOND INTO A SPECTRUM OF FATTY ACYL-COA SUBSTRATES AMONG WHICH PALMITOYL-COA AND STEAROYL-COA (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Stearoyl-CoA + AH(2) + O(2) = oleoyl-CoA + A + 2 H(2)O.
 CC -1- COFACTOR: IRON.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic reticulum (Probable).
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE AND/OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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or send an email to license@isb-sib.ch).

CC EMBL: AF186710; AAF22305.1; -
 DR InterPro: IPR001522; Desaturase.
 DR Pfam: PF01069; Desaturase; 1.
 DR PRINTS: PR00075; FADCDSATRASE.
 DR ProDom: PD002221; Desaturase; 1.
 DR PROSITE: PS00476; FATTY ACID DESATUR-1; 1.
 KW Oxidoreductase; Fatty acid biosynthesis; Transmembrane;
 KM Endoplasmic reticulum; Iron.
 FT TRANSMEM 76
 FT TRANSMEM 98
 FT TRANSMEM 118
 FT TRANSMEM 223
 FT TRANSMEM 243
 FT TRANSMEM 315
 FT TRANSMEM 335
 FT DOMAIN 120
 FT DOMAIN 157
 FT DOMAIN 161
 FT DOMAIN 296
 FT DOMAIN 302
 FT SEQUENCE 359 AA; 41755 MW; 22FB69BD1846C3 CRC64;

Query Match 17.7% Score 343.5; DB 1; Length 359;
 Best Local Similarity 28.3%; Pred. No. 1.3e-22;
 Matches 104; Conservative 52; Mismatches 145; Indels 67; Gaps 11;

15 LSEAMASFIATTPPAMPAPASVLD-----PKIP-----TKPEPK-----TET 52
 6 LOEIISSYTTTITPAP-SRVLONGGKLEKTPYLEEDIRPEKRDIDYPTODKEG 64
 53 PKRPDDERRRTSVVLEERSKSGFWRKRNPRDIONAVTLVLHALLA-----AMAPFFSM 108
 65 PKPK-----LEY-----VWR-----NIIIMSLHLAGALGILLPTCKIY 99
 109 DAFWISFILLGASVGLITLCEHRLTHGGFKLPKLYEYFAVCGSLALOGDPMEMVSN 168
 100 TYIVLFYYL--MGALGITAGAHRLMSHTYKARLEPLRFELIYGNMAFQNDVFEMSRD 156
 169 HRYHQFVDERDVHSPVQGFWRPCHIGWVL-DKDLFEYKRGRRNNVNDLKKQAFRELOK 228
 157 HRAHNFSETDADHNSRGRFFSHVGMVLVYKRPVAVKEKSTLNLSDLAEKLYVFOR 216
 229 TYMHQALALILLYYVGFYIWMGFRIVFMF-----HSTFAINSYCHKWGR 278
 217 YKPGVILLCTILPTL--VPMYLMDETFONSLEPFLRYALGLNVTWLVNSAHLWGYR 274
 279 PWNFGDLSTNNMFYALCAFEGSGMNNHAFEGSARHGLEWMOIDVTWYVIRLQATGLAT 338
 275 PYDKTINRENILVSLGAVGEGFNHYHFFPYDYSASEYRMHINTLTFIDCMAALGLAY 334
 339 NVKLPTEA 346
 335 DRKAKSKA 342

RESULT 6
 ACOD_MESAU STANDARD; PRT; 354 AA.

AC 064420;
 15-JUL-1998 (Rel. 36, Created)
 15-JUL-1998 (Rel. 36, Last sequence update)
 16-OCT-2001 (Rel. 40, Last annotation update)
 Acyl-CoA desaturase (EC 1.14.99.5) (Stearoyl-CoA desaturase) (Fatty acid desaturase) (Delta(9)-desaturase).
 SCD OR FAR-17C.
 OS Mesocricetus auratus (golden hamster).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 CC Mesocricetus.
 CC NCBI_TaxID=10036;
 RN SEQUENCE FROM N.A.
 RP MEDLINE=95290467; PubMed=7772580;
 RX Medline R., Seki T., Adachi K.;
 RA "Sequence analysis and characterization of FAR-17C, an androgen-


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RT dependent gene in the flank organs of hamsters."
CC J. Dermatol. Sci. 9:94-102(1995).
CC
CC -1- FUNCTION: TERMINAL COMPONENT OF THE LIVER MICROSOomal STEARYL-COA
CC DESATURASE SYSTEM, THAT UTILIZES O(2) AND ELECTRONS FROM REDUCED
CC CYTOCHROME B(5) TO CATALYZE THE INSERTION OF A DOUBLE BOND INTO A
CC SPECTRUM OF FATTY ACYL-COA SUBSTRATES AMONG WHICH PALMITOYL-COA
CC AND STEAROYL-COA (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Stearoyl-CoA + AH(2) + O(2) -> oleoyl-CoA + A +
CC 2 H(2)O.
CC -1- COFACTOR: IRON.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum (Probable).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: L26956; AAC42058.1; -
CC DR InterPro: IPR001522; Desaturase.
CC DR Pfam: PF01069; Desaturase; 1.
CC DR PRINTS: PR00075; FADDSATRASE.
CC DR PRODOM: PD002221; Desaturase; 1.
CC DR PROSITE: PS00476; FATTY_ACID_DESATUR_1; 1.
CC DR Oxidoreductase: Fatty acid biosynthesis; Transmembrane:
CC KM Endoplasmic reticulum; Iron.
CC FT TRANSMEM 71 91 POTENTIAL.
CC FT TRANSMEM 93 113 POTENTIAL.
CC FT TRANSMEM 218 238 POTENTIAL.
CC FT TRANSMEM 310 330 POTENTIAL.
CC FT DOMAIN 115 120 HISTIDINE BOX 1.
CC FT DOMAIN 152 156 HISTIDINE BOX 2.
CC FT DOMAIN 293 297 HISTIDINE BOX 3.
CC SO SEQUENCE 354 AA; 40968 MW; B41A0831845EB874 CRC64;

Query Match 17.6%; Score 342; DB 1; Length 354;
Best Local Similarity 26.9%; Pred. No. 1.7e-22;
Matches 98; Conservative 61; Mismatches 141; Indels 64; Gaps 13;

QY 15 LSLIEMASTIATTTTPAMPAPASYLDKIP-----TKPEPK-----TETPKKDD 58
DB 6 LQSEMTSYTTTTTTEPPSESIQKTVPLYLEDIRPEMKEDIYPSYQDEGPPPK-- 63
QY 59 LERFRTSEVVLERKSKGFPRRRKNRPDIOMNAVTLVLVLAALA-----AMAPFTYSMDAFWIS 114
DB 64 -----Ley-----VVR-----NIIMLALHLAGYLGLVLPSSKYYTLIM-A 99
QY 115 FILLGASGVLTGTLCTHGHCLTHGFKLPKLYEYFPAVCGSIALOGDPPENYSHRYHHO 174
DB 100 FYV--YVIEIGAGVAVHMLSHRYTKARLPRIPLITANTAFQVDYEMARDHAHAK 157
QY 175 FVDTEDVHSPTQGEWECHIGVNL-DKDLFVERGRGRNNVNDLKKQAFRYFLQKTYMH 233
DB 158 FSETYADPHDSRRGFESHVGMVLVLRKHPAVKEGKGL-DMSDLNKEKLVYQRR---Y 213
QY 234 QIALIALLLVYVCGF-PYIWMGCF-----RLVFPFHSFPAINSYCHKMGKGPWNT 282
DB 214 KPIILMCYTLPLFVFWYWGAFVNSLCVSTFLRYTLVLTWLVNSAAHLYGYRPPYDK 273
QY 283 GDLSTNMFVALCAGFEGVHNNHAFEGSARHGLEWMOIDVWYVYRTQATIGLATNVYL 342
DB 274 NIDPRNALVSLGCLGEGHNHNAFPRYDYSASBYRWHNINFTTFIDCAALGLAYDRKK 333
QY 343 PTBA 346
DB 334 VSKA 337

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RESULT 7
ID ACOD_HUMAN STANDARD; PRT; 359 AA.
AC 000767; Q16150; Q9Y695;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Acyl-CoA desaturase (EC 1.14.99.5) (Stearoyl-CoA desaturase) (Fatty
DE acid desaturase) (Delta(9)-desaturase).
GN SCD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Al-Jeyan L., Mccord A., Pierotti A.R., Craft J.A.;
RN Submitted (JUN-1997) to the EMBL/Genbank/DBJ databases.
RP SEQUENCE FROM N.A.
RC TISSUE=Liver, Brain, and Skin;
RX MEDLINE=99247918; PubMed=10229681;
RA Zhang L., Ge L., Parimoo S., Stenn K., Prouly S.M.;
RT "Human stearoyl-CoA desaturase: alternative transcripts generated from
RL a single gene by usage of tandem polyadenylation sites."
RN Biochem. J. 340:255-264(1999).
RP SEQUENCE FROM N.A.
RA Hoshino T., Ohtsu K.;
RT "Cloning, sequencing and expression of human stearoyl-CoA
RT desaturase."
RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE OF 3-239 FROM N.A.
RC TISSUE=Adipose tissue;
RX MEDLINE=94222609; PubMed=7909540;
RA Li J., Ding S.-F., Habib N.A., Fermor B.F., Wood C.B., Gilmour R.S.;
RT "Partial characterization of a cDNA for human stearoyl-CoA desaturase
RT and changes in its mRNA expression in some normal and malignant
RT tissues."
RL Int. J. Cancer 57:348-352(1994).
CC -1- FUNCTION: TERMINAL COMPONENT OF THE LIVER MICROSOomal STEARYL-COA
CC DESATURASE SYSTEM, THAT UTILIZES O(2) AND ELECTRONS FROM REDUCED
CC CYTOCHROME B(5) TO CATALYZE THE INSERTION OF A DOUBLE BOND INTO A
CC SPECTRUM OF FATTY ACYL-COA SUBSTRATES AMONG WHICH PALMITOYL-COA
CC AND STEAROYL-COA.
CC -1- CATALYTIC ACTIVITY: Stearoyl-CoA + AH(2) + O(2) -> oleoyl-CoA + A +
CC 2 H(2)O.
CC -1- COFACTOR: IRON.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum (Probable).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: Y13647; CAA73998.1; -
CC DR EMBL: AF097514; AAD29870.1; -
CC DR EMBL: AB032261; BAA93510.1; -
CC DR EMBL: S70284; AAB30631.1; -
CC DR MIM: 604031; -
CC DR InterPro: IPR001522; Desaturase.
CC Pfam: PF01069; Desaturase; 1.

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Query Match	16.9%	Score 329.5	DB 1	Length 358
Best Local Similarity	28.98	Pred. No. 2.1e-21		
Matches 90	Conservative 55	Mismatches 133	Indels 33	Gaps 9
53 PKPDDL-EERRFSEVLLERKSKGFRKKNPNRDIQNAVVLVLAHALA---AAAPRYF 106	1:	1:	1:	1:
47 PELKDDLDPYQDDGGR-PRKLEVVNR-----NIIIMALLHIGALVGITLVP-- 93	1:	1:	1:	1:
107 SWDAFWISFILGRASGVGLITLCPHRLITGGRFLPLVLEYEFFRAYGCSLALQSPRMENV 166	1:	1:	1:	1:
94 SCKLYTCLFAVLYLVYISALGITAGAHRLMSHRTYKARPLRLFLIIANTMAFQNDVUYEFA 153	1:	1:	1:	1:
167 SNHRYHNOFVTERDVHSPRTQGFMECHLAWL-DKDLFEVERKGRNRNVNDIKKQAFYRF 225	1:	1:	1:	1:
154 RDHANHNKFTSHADPHNRSGRGFPSHNGWLLVLRKNHRAVKEKGGCL-DMSDLKAKKLWVF 212	1:	1:	1:	1:
226 LQKTYMTHQALALLLVYVGGFRYYIVWGMG-----RLVMEHSTPAINSVCHKW 275	1:	1:	1:	1:
213 QRRYYKPDLLIMCFVLPTL--VPMWCGSEFTVNSLCVSTFLRYAVAVLNAWTWLVNSAAHLX 270	1:	1:	1:	1:
276 GGRPWNTGDLSTNNMFVNLCAFGEGWHNNHNAFEDSAHNGLEMMQIDTWVYVIRPLQALG 335	1:	1:	1:	1:
271 GYRPDKNISSRENTLVMSGAVGERFHNHNAFPDYIASERWHTINFTTFIDCMALIG 330	1:	1:	1:	1:
336 LATWKLPTFA 346	1:	1:	1:	1:
331 LAYDKRKVSRA 341	1:	1:	1:	1:

RESULT 9
ACOL_YEAST STANDARD: PRT: 510 AA.
ID ACOL_YEAST
P21147;
01-MAY-1991 (Rel. 18, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DE Acyl-CoA desaturase 1 (EC 1.14.99.5) (Stearoyl-CoA desaturase 1)
GN (Fatty acid desaturase 1).
OLE1 OR YGL055W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OX Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_Taxid=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91056050; PubMed=1978720;
RA Stucky J.E., McDonough V.M., Martin C.E.;
RT "The OLE1 gene of *Saccharomyces cerevisiae* encodes the delta 9 fatty
RT acid desaturase and can be functionally replaced by the rat stearoyl-
RT CoA desaturase gene."
RL J. Biol. Chem. 265:20144-20149(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=5288C;
RX MEDLINE=97377993; PubMed=9234674;
RA Feuerhahn M., de Montigny J., Potler S., Souciet J.-L.;
RT "The characterization of two new clusters of duplicated genes
RT suggests a 'Lego' organization of the yeast *Saccharomyces cerevisiae*
RT chromosomes."
RL Yeast 13:861-869(1997).
CC -1- FUNCTION: UTILIZES O(2) AND ELECTRONS FROM THE REDUCED CYTOCHROME
CC B(5) DOMAIN TO CATALYZE THE INSERTION OF A DOUBLE BOND INTO A
CC SPECTRUM OF FATTY ACYL-CoA SUBSTRATES (PROBABLE).
CC -1- CATALYTIC ACTIVITY: Stearoyl-CoA + AH(2) + O(2) -> oleoyl-CoA + A +
CC 2 H(2)O.
CC -1- COFACTOR: IRON.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum (Probable).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC -1- SIMILARITY: CONTAINS A CYTOCHROME B5 FAMILY, HEME-BINDING DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: J05676; AAA34826.1; -
CC EMBL: 272577; CAA96757.1; -
CC PIR: A23675; A23675.
DR SCD, S0003023; OLE1.
DR InterPro: IPR001199; CytL-B5.
DR Pfam: PF01069; Desaturase.1.
DR PRINTS: PR00075; FADDSATURASE.
DR PRODOM: PD002221; Desaturase.1.
DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE: PS00476; FATTY_ACID_DESATUR_1; 1.
DR OXidoreductase; Fatty acid biosynthesis; Iron; Electron transport;
KM Transmembrane; Endoplasmic reticulum; Heme.
FT TRANSMEM 113 133 POTENTIAL.
FT TRANSMEM 139 159 POTENTIAL.
FT TRANSMEM 236 276 POTENTIAL.
FT DOMAIN 281 301 POTENTIAL.
FT DOMAIN 161 166 HISTIDINE BOX 1.
FT DOMAIN 198 202 HISTIDINE BOX 2.

FT DOMAIN 335 339 HISTIDINE BOX 3.
FT DOMAIN 409 487 HEME-BINDING.
FT BINDING 444 444 HEME LIGAND (BY SIMILARITY).
FT BINDING 470 470 HEME LIGAND (BY SIMILARITY).
FT CONFLICT 304 304 L -> M (IN REL. 1).
SO SEQUENCE 510 AA; 58403 MW; A6CC78DD4210ECCA CRC64;

Query Match 16.8%; Score 326; DB 1; Length 510;
Best Local Similarity 29.5%; Pred. No. 6.3e-21;
Matches 83; Conservative 50; Mismatches 114; Indels 34; Gaps 8;

QY 97 ALAAMPFYSSNAPFISFLILGFASGVLCITCFRHCILTHGKFLPKLYEFPATCGSL 156
DB 130 ALGKVPFLHNVLFVSYFY---YAVGVSITAGYHRLMHSRSYSAHPRLFLYATFGCA 185
QY 157 ALGGDPMEVSNRHYHOFEDTERDVSPGQGFICIGVLLKDKLVEKGRGRNNVND 216
DB 186 SVGSAKMGHSHRHHRYDTLRDPDARGILMSMGMLKLP---NPKYARADYTD 242
QY 217 LKKQAFYRFLQKTYMYHQI-----ALIALLY---YVGGFPYIWMGFRFLVFMF-HST 265
DB 243 MTDQWTIRFQHRHYILLMLTAFAVYPTLCGYFFENDYMGGLY---AGFIRFVIGQAT 298
QY 266 FAINSYCHKKMGGRPMNTGDLSTNNMFALCAFEGBGNNHNAFEQSRHGLEMMQIDYTW 325
DB 299 FCINSLSAHYIGTGFEDRRTPTDMMITAIYTFEGGHNHFHEPPTDYRNAIKMYOYDPTK 358
QY 326 YVIRTLQALIGLATNVK-----LPTBAKQ--KLKAK 354
DB 359 VVILNLSVLADLKDFFSQNALIEALIQEOKKINKKKK 399

RESULT 10
FD3C_BRANA STANDARD: PRT: 404 AA.
ID FD3C_BRANA
AC P48618;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Omega-3 fatty acid desaturase, chloroplast precursor (EC 1.14.99.-)
DE (Fragment).
GN PAD7.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Brassica.
OX NCBI_Taxid=3708;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Seed;
RX MEDLINE=94302147; PubMed=8029334;
RA Yadav N.S., Wierzbicki A., Aegerter M., Caster C.S., Perez-Grau L.,
RA Kliney A.J., Hitz W.D., Booth J.R., Jr., Schweitzer B., Stecca K.L.,
RA Allen S.M., Blackwell M., Reiter R.S., Carlson T.J., Russell S.H.,
RA Feldman K.A., Pierce J., Browne J.;
RT "Cloning of higher plant omega-3 fatty acid desaturases."
RT Plant Physiol. 103:467-476(1993).
CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC -----
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EMBL: L22963; AAA61774.1; ALT_INIT.
 DR PIR: P00812; P00812.
 DR InterPro: IPR001225; FA_desaturase.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR ProDom: PD001081; FA_desaturase; 1.
 DR Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
 KW Transit peptide.
 FT NON_TER 1
 FT TRANSIT 1
 FT CHAIN <1 ? CHLOROPLAST (POTENTIAL).
 FT DOMAIN 121 404 OMEGA-3 FATTY ACID DESATURASE.
 FT DOMAIN 157 161 HISTIDINE BOX 1.
 FT DOMAIN 324 328 HISTIDINE BOX 2.
 FT DOMAIN 324 328 HISTIDINE BOX 3.
 SEQUENCE 404 AA; 46617 MW; 4B58FB2F36E2ED4 CRC64;

Query Match 5.7%; Score 111.5; DB 1; Length 404;
 Best Local Similarity 23.6%; Pred. No. 0.022;
 Matches 83; Conservative 44; Mismatches 98; Indels 127; Gaps 27;

OY 43 PTKPEPKTE-----TPKPKDLERRTSEVYLERKS--KGFWRKRNPRDIONAVT--LL 93
 DB 36 PLEEDPKTORPDGAPPP-----FNLADI---RAAIKPHCVK--NPKKMSYVVRRLA 84
 OY 94 VHAALAAAPF---YESMDAFWISFLILGASGVIGITLCFRCILHGGF-----LTKPIY 146
 DB 85 IYFALAGAAIYNNWLVPLIYAGTGMWALFVLG-----HDC-GHGSFSDPRLNSVY 138
 OY 147 EYFAYCGSLALGDPMEVSNHRYHQ---FVDERDVH-----SPTGFWFC 192
 DB 139 GHLLSSILVPHYG---WRISHRTHQNHGVENDESMHPSSEKITYSLDKPTPFREF 194
 OY 193 -----HIGWVL-----DKDLPEKRGGRNNVNDLKKQAFYFLQKTYW 232
 DB 195 LPLVLAAYPYLIWARSPEKKGSHYHDSDLFLPK---ERNVD-----LITSTACW 240
 OY 233 HOLA-LIALIYVVG-----PPY---IYWGMGFLVGFHSTFAINSVCHK----- 274
 DB 241 TAMAVLLVLCINLVNPMQMLKIYLPYMINVM-LDF-VTYIHNG-----HEDKLPW 291
 OY 275 WGRFPMW--TGDLST-----NNMEVALCAFEGEGHNNHAFQGSARHGL 316
 DB 292 YRGKEMSYLRGGLTTLDRDYGLINNIIHDI-----GTIVIHHLFPQIDPHYHL 338

RESULT 11
 FD3C_ARATH STANDARD; PRT; 446 AA.
 AC P46310;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Omega-3 fatty acid desaturase, chloroplast precursor (EC 1.14.99.-).
 GN FAD7 OR FADD OR AT3G11170 OR F9F8.4 OR F11B9.10.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, COLUMBIA; TISSUE=Hypocotyl;
 RX MEDLINE=94302147; PubMed=8029334;
 RA Yadav N.S., Wierzbicki A., Aegerter M., Caster C.S., Perez-Grau L.,
 RA Kinney A.J., Hitz W.D., Booth J.R., Jr., Schweiger B., Stecca K.L.,
 RA Allen S.M., Blackwell M., Reiter R.S., Carlson T.J., Russell S.H.,
 RA Feldmann K.A., Pierce J., Browne J.,
 RT "Cloning of higher plant omega-3 fatty acid desaturases";
 RL Plant Physiol. 103:467-476(1993).

[2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=CV, COLUMBIA; TISSUE=Aerial parts;
 RC MEDLINE=94043239; PubMed=8226956;
 RX Iba K., Gibson S., Nishuchi T., Fuse T., Nishimura M., Arondel V.,
 RA Hugly S., Somerville C.R.;
 RT "A gene encoding a chloroplast omega-3 fatty acid desaturase
 RT complements alterations in fatty acid desaturation and chloroplast
 RT copy number of the fad7 mutant of Arabidopsis thaliana";
 RL J. Biol. Chem. 268:24099-24105(1993).

[3]
 RN SEQUENCE FROM N.A.
 RP STRAIN=CV, COLUMBIA; TISSUE=Hypocotyl;
 RC Watahiki M., Yamamoto K.;
 RL submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
 [4]
 RN SEQUENCE FROM N.A.
 RC STRAIN=CV, COLUMBIA;
 RX MEDLINE=21016720; PubMed=11130713;
 RA Salanoubat M., Lemcke K., Rieger M., Ansoer W., Unsel M.,
 RA Farman B., Valle G., Bloeker H., Perez-Alonso M., Obermayer B.,
 RA Delzeny M., Boutry M., Grivell L.A., Maché R., Puigdomenech P.,
 RA De Simone V., Choise N., Artiguenave F., Robert C., Brottier F.,
 RA Winkler P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
 RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
 RA Wüdelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
 RA Verzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
 RA Corrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,
 RA Reichelt J., Scharfe M., Schoen O., Barues M., Terol J., Climent J.,
 RA Navarro P., Collado M., Perez-Perez A., Ottenwelder B., Duchemin D.,
 RA Cooke R., Laudie M., Beger-Liaou C., Purrelle B., Masuy D.,
 RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
 RA Monfort A., Argitrou A., Flores M., Lignori R., Vitale D.,
 RA Mannhaupt G., Haase D., Schoof H., Rüd S., Zaccaria P., Mewes H.-W.,
 RA Meyer K.F.X., Kaul S., Town C.D., Koo H.L., Talon L.J., Jenkins J.,
 RA Rooney T., Rizzo W., Wals A., Uteirack T., Fujii C.Y., Shea T.P.,
 RA Creasy T.H., Haas B., Malt R., Wu D., Peterson J., Van Aken S.,
 RA Pal G., Miltischer J., Sellers P., Gill J.E., Feldlyum T.V.,
 RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
 RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
 RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,
 RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
 RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
 RT thaliana";
 RL Nature 408:820-822(2000).

-1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
 THE THIRD DOUBLBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
 ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
 TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
 -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
 -1- TISSUE SPECIFICITY: MOST ABUNDANT IN LEAVES AND SEEDLINGS.
 -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 AND/ OR BE INVOLVED IN METAL ION BINDING.
 -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.

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CC EMBL: L22961; AAA61774.1; -;
 DR EMBL: D14007; BAA03106.1; -;
 DR EMBL: D26019; BAA05040.1; -;
 DR EMBL: AC009991; AAF01508.1; -;
 DR EMBL: AC073395; AAG50977.1; -;

DR InterPro: IPR001225; FA_desaturase.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR ProDom: PD001081; FA_desaturase; 1.
 KW Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
 KM Transit peptide.
 FT TRANSIT 1 2 CHLOROPLAST (POTENTIAL).
 FT CHAIN 1 446 OMEGA-3 FATTY ACID DESATURASE.
 FT DOMAIN 163 167 HISTIDINE BOX 1.
 FT DOMAIN 199 203 HISTIDINE BOX 2.
 FT DOMAIN 366 370 HISTIDINE BOX 3.
 SQ SEQUENCE 446 AA; 51174 MW; 121125F634553D35 CRC64;

Query Match 5.6%; Score 108.5; DB 1; Length 446;
 Best Local Similarity 22.0%; Pred. No. 0.045;
 Matches 89; Conservative 47; Mismatches 121; Indels 147; Gaps 28;

QY 1 LRSLKFPISISLSLEMAAF-----IATTP-AMPAASVLDKIKTPKPKETK 54
 DB 36 LSSSTKSTSSPLSGFNSHOGFTRMALMVSTPLTPIF-----ESPL 80
 QY 55 PKDLERFRTSEV-----VLERKSKGFV-RKKMP-----RDIONAVTLVLALAM 101
 DB 81 EEDNKRQFDPGAPPENLADIRAIKHKVKKPKSKLSVAVDY-----AIVFALAG 134
 QY 102 APP---YFSDAFWISFILLGFRASGVLTLCRHRLTHGCF---KLPKLYEYFAYCG 154
 DB 135 AALNWMIVPRLVLAOGTFMALFVLG-----HDC-GHGSFSDNKLKLSVGHLSHSI 188
 QY 155 SLALOGDPMKWNVSNHRYHNO---FVDERDVH-----SPNQGWFEC----- 192
 DB 189 LVPYHG---WRISHTHNOHGHVNDSEWHPMSKITYNTLDKPRFRFRLPLVLMAY 244
 QY 193 -HIGVVL-----DKDLFEVERKGRNNVNDLKQAFYRFLQKTYMYHOLA--LI 238
 DB 245 PFYLMARSPGKSGHYHPSDLELPK---ERKDV-----LTSTACMTAMALLV 290
 QY 239 ALLYVG-----GFRY---IYMGGRFLVPMFSTALNSVCKK-----WGRPMN- 281
 DB 291 CLAFETGPIOMLKLYGIPWINVM-LDF-VYULHNG-----HEDKLPWYRKEMSY 341
 QY 282 -TGDIST-----NNMFVALCAFGEGMNNHAFQOSARHGL 316
 DB 342 LMGGLTTLDRDYGLINNIHDI-----GTHVHHLFQRLPHYHL 380

RESULT 12
 FD3E_PHAU
 ID FD3E_PHAU STANDARD; PRT; 380 AA.
 AC P32291;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Omega-3 fatty acid desaturase, endoplasmic reticulum (EC 1.14.99.-)
 DE (Indole-3-acetic acid induced protein ARG1).
 GN ARG1.
 OS Phaseolus aureus (Mung bean) (Vigna radiata).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
 OX NCBI_TaxID=3916;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=hypocotyl;
 RA Yamamoto K.T., Mori H., Imaseki H.;
 RT "Novel mRNA sequences induced by indole-3-acetic acid in sections of
 RT elongating hypocotyls of mung bean (Vigna radiata).";
 RL Plant Cell Physiol. 33:13-20(1992).
 CC -1- FUNCTION: MICROSMAL (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
 CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
 CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
 CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER

CC PHOSPHOLIPIDS.
 CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum.
 CC -1- INDICATION: BY AUXIN, ETHYLENE AND WOUNDING.
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 CC AND/OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: D14410; BAA03306.1; -
 DR InterPro: IPR001225; FA_desaturase.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR ProDom: PD001081; FA_desaturase; 1.
 KW Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
 KM Transmembrane.
 FT TRANSMEM 59 78 POTENTIAL.
 FT TRANSMEM 208 231 POTENTIAL.
 FT TRANSMEM 238 256 POTENTIAL.
 FT DOMAIN 97 101 HISTIDINE BOX 1.
 FT DOMAIN 133 137 HISTIDINE BOX 2.
 FT DOMAIN 300 304 HISTIDINE BOX 3.
 SQ SEQUENCE 380 AA; 43996 MW; 1C005117A8DAE168 CRC64;

Query Match 5.4%; Score 105; DB 1; Length 380;
 Best Local Similarity 21.6%; Pred. No. 0.076;
 Matches 77; Conservative 38; Mismatches 105; Indels 136; Gaps 21;

QY 36 SYLDKRIPIK---PEPKTPKPKDLEFRFRTSEVLERKSKGWRKKMPPDIONAVTL 92
 DB 20 SYFDPAPPPEFIADIRAIKPKHCKEKTSLRSLSYL-----BDV----- 59
 QY 93 LVILHALAAMA---PYFSDAFWISFILLGFRASGVLTLCRHRLTHGCF---KLPK 145
 DB 60 LVYTLAASAIISFNKSTFPLYPKAGTFMALFVLG-----HDC-GHGSFSSKLSNF 113
 QY 146 VEYFAYCGSLALOGDPMKWNVSNHRYHNO---FVDERDVHSPYQGFHIGV-LDKDLF 203
 DB 114 VGHILSLTLVYNG---WRISHTHNOHGHVNDSEWHPMSKITYNTLDKPRFRFRLPHYHL 157
 QY 204 VEKRGGRNNVNDLKQAFYR-----FLQKTYMYHNO----- 234
 DB 158 -----KNLDDMTMLRYSPPPIFAVRYFLMNRSPGKSGHNPYSNLFSPGERKV 209
 QY 235 -----LALIALYU---VG-----GPRYIYMGGRFLVPMFSTALNSVCKK- 274
 DB 210 VSTLCKGIVLSVLLXSLTITPIIMLKLYGYPYLIIFWMLDFYULNH---HGYTHKL 265
 QY 275 -WGRPMN--TGDISTNNMFVALCAFGEGMNN-----HNAFQOSARHGL 316
 DB 266 PMYRQGEWSYLRGLTYDR-----DYGWINNVNHDIGTHVHHLRPHYHL 314

RESULT 13
 FD3C_RICCO
 ID FD3C_RICCO STANDARD; PRT; 460 AA.
 AC P48619;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Omega-3 fatty acid desaturase, chloroplast precursor (EC 1.14.99.-).
 DE FAD7A-1.
 GN Ricinus communis (Castor bean).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Malpighiales; Euphorbiales; Ricinus.

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OX NCBI_Taxid=3988;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, BAKER 296; TISSUE=seed;
RX MEDLINE=94302177; PubMed=8029360;
RA van de Ioo F.J., Somerville C.R.;
RT "Plasmod omega-3 fatty acid desaturase cDNA from Ricinus communis.";
RL Plant Physiol. 105:443-444(1994).
CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS. IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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CC -----
DR EMBL; L25897; AAA73511.1; -.
DR InterPro: IPR001225; FA_desaturase.
DR Pfam; PF00487; FA_desaturase; 1.
DR ProDom; PD001081; FA_desaturase; 1.
KW Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
KW Transit peptide.
FT CHAIN 1 ? ? CHLOROPLAST (POTENTIAL).
FT TRANSIT 1 ? OMEGA-3 FATTY ACID DESATURASE.
FT DOMAIN 177 181 HISTIDINE BOX 1.
FT DOMAIN 213 217 HISTIDINE BOX 2.
FT DOMAIN 380 384 HISTIDINE BOX 3.
SQ SEQUENCE 460 AA; 52561 MW; 836592904EF3C7B0 CRC64;

Query Match 5.1%; Score 99; DB 1; Length 460;
Best Local Similarity 20.8%; Pred. No. 0.31;
Matches 75; Conservative 42; Mismatches 106; Indels 138; Gaps 19;

OY 52 TPKPDDLEERTSEVLEERKSKGFWRRKWP-----RDIONAV----- 90
DB 76 TVSGDDDEREFNGIVWDEKGEFFDAGAPRPTLDIRAIGKHCVKWPMSMSYV 135
OY 91 --TLVLHALAAMAPFYSSMDA---FWISFILLGFASGYLGITLGFHRCILTHGGF---K 141
DB 136 LRDVVVVGGLAAVAAYFNNWVAMPPLWFCQGTMFVALFVLG-----HDC-GHGSFSNNPK 189
OY 142 LPKLVEYFAYCGSLALGDPMWVSNHRYHNO---FVDTEDVHSPGQGFV----- 190
DB 190 LNSVGGHLLHSSILVPRHG---WRISHRTNHQNGHVENDSWHPLEKITYKSLDNYTK 245
OY 191 -----FCHIGWVL-----DKDLFEVERKGRGRNNVNDLKKQAFYRELQ 227
DB 246 TLRFSLPRLALYPRYLMSRSPGKGSHPHDSGLFVPR-----ERKDI-----IT 291
OY 228 KTYMTHTALATLLTYVG-----GPRYTWGSGFVLVWFHSTFAINSYCHK- 274
DB 292 STACW--TAMAAALVYLNFSGMPVOMLKYGIPIYFIWMDLDFVLYLH-----HHG 340
OY 275 -----WGGRPMN--TGDLSTNNMFVALCAFGEGMHNH-----HHAFEQSARHG 315
DB 341 HEDKLPMTRGKMSYLRGGLTLDR-----DYGMINNHHIDIGTNYIHLLFPOLPRYH 393
OY 316 L 316
DB 394 L 394

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RESULT 14
FD3C_SESIN
ID FD3C_SESIN STANDARD; PRT; 447 AA.
AC P48620;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Omega-3 fatty acid desaturase, chloroplast precursor (EC 1.14.99.-).
GN FAD7.
OS Sesamum indicum (Oriental sesame) (Ginelly).
OC Eukaryota; Viridiplaneta; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; easterids I; Lamiales; Pedaliaceae; Sesamum.
OX NCBI_Taxid=4182;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, 4294; TISSUE=Cotyledon;
RA Shoji K.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS. IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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CC -----
DR EMBL; U25817; AAA70334.1; -.
DR InterPro: IPR001225; FA_desaturase.
DR Pfam; PF00487; FA_desaturase; 1.
DR ProDom; PD001081; FA_desaturase; 1.
KW Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
KW Transit peptide.
FT CHAIN 1 ? ? CHLOROPLAST (POTENTIAL).
FT TRANSIT 1 ? OMEGA-3 FATTY ACID DESATURASE.
FT DOMAIN 167 171 HISTIDINE BOX 1.
FT DOMAIN 203 207 HISTIDINE BOX 2.
FT DOMAIN 370 374 HISTIDINE BOX 3.
SQ SEQUENCE 447 AA; 51116 MW; 4E76250DD6DA6B1 CRC64;

Query Match 5.1%; Score 98.5; DB 1; Length 447;
Best Local Similarity 22.3%; Pred. No. 0.33;
Matches 79; Conservative 31; Mismatches 101; Indels 143; Gaps 23;

OY 43 PTKPEKTEPRKDDLEERTSEVLEERKSKGFV-RRKWP-----RDIONAVTLLVLH 96
DB 94 PGAPRP-----FKLSD-IRRAIPKHCWVKWPMRSMGYVADV-----AVVF 133
OY 97 ALAAMAAPFYPS--WDATWISFILLGFASGYLGITLGFHRCILTHGGF---KLPKLYEYF 149
DB 134 GLAAVAAYFNNWVAPLWLFQOSTMFVALFVLG-----HDC-GHGSFSDPKLNSVGH 187
OY 150 FAYCGSLALGDPMWVSNHRYHNO---FVDTEDVH-----KLPKLYEYF 183
DB 188 LHSSTLVPRHG---WRISHRTNHQNGHVENDSWHPLEKITYKSLDNYTK 243
OY 184 -----SP-TGQFWFCHIGWVLDDKDLFEVERKGRGRNNVNDLKKQAFYRELQ 230
DB 244 PLLAVPYLMSRSPGKGSHP-H-----PDSDLFVYNE-----KKDVTSTVCWTA 288

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OY 221 MYHOLALALALYYVG-----GPPYIWMGGRFLVMEFSTRAINSVCHK----- 274
DB 268 ML--ALLVGLSPVIGIPVOLKLKYGIPYLGNYMMWLDLYLH-----HHGHEDKLPW 337
OY 275 WGRFPMN--TGDLSTNNMFVALCAFGEGMHN-----HHAFGSARHG 316
DB 338 YRGKMSYLRGLTLTDR-----DYGMINNIHHDGTHVHILFQIPHYHL 384

RESULT 15
FD3D_ARATH STANDARD: PRT: 435 AA.
AC P48622:
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Temperature-sensitive omega-3 fatty acid desaturase, chloroplast
DE precursor (EC 1.14.99.-).
GN FAD8 OR AT5G05580 OR MOP10.12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA; TISSUE-Aerial parts;
RX MEDLINE=95148742; PubMed=7846164;
RA Gibson S., Arondel V., Ida K., Somerville C.R.;
RT Cloning of a temperature-regulated gene encoding a chloroplast
RT omega-3 desaturase from Arabidopsis thaliana."
RL Plant Physiol. 106:1615-1621(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA; TISSUE-Hypocotyl;
RA Wataniki M.C., Yamamoto K.T.;
RT Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. Columbia;
RX MEDLINE=97471969; PubMed=9330910;
RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
RA Miyajima N., Tabata S.;
RT Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
RT features of the 1.6 Mb regions covered by twenty physically assigned
RT pl clones."
RL DNA Res. 4:215-230(1997).
CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST; MEMBRANE-BOUND (PROBABLE).
CC -1- INDUCTION: BY LOW TEMPERATURE.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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CC -----
DR EMBL: L27158; AA65621.1; -
DR EMBL: U08216; AAB60302.1; -
DR EMBL: D17578; BAA04504.1; -
DR EMBL: AB005241; BAB11547.1; -
DR InterPro: IPR001225; FA_desaturase.
DR Pfam: PF00487; FA_desaturase; 1.

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DR Prodom: PD001081; FA_desaturase; 1.
KW Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
KW Transil peptide.
FT TRANSIT 1
FT CHAIN 1
FT FT 435
FT DOMAIN 156
FT DOMAIN 192
FT DOMAIN 359
FT SEQUENCE 435 AA; 50136 MW; 3D77A8035A6214E1 CRC64;

Query Match 4.9%; Score 95.5; DB 1; Length 435;
Best local Similarity 20.8%; Pred. No. 0.59;
Matches 75; Conservative 37; Mismatches 104; Indels 145; Gaps 21;

OY 48 PKTETPKP-KDLEPRRTSEVYLERKSGFWRKKNPRDIQNAV----- 90
DB 66 PLTTTQSPSEEDTERPDGCA-----PPFLADIRAIRKHCWVKPMMSSTV 114
OY 91 --TLVLHLHLMAMPY---FSWDAFWISFILLGASGVLTLCFHRCTHGF---K 141
DB 115 VQDVATVGLAAVALENNWMLMPLYWFAQGMFVALFVLG---HDC-GHGSPNDPR 168
OY 142 LPLVYEFPAVCGSLALQGDPMENVSNNRYHQ---FVDEEDVH-----SPTQ 187
DB 169 LMSVAGHLHSSILVPYHG---WLSHRTIHQNHGVENDSWHPLDPSYKMLEKTQ 224
OY 188 GWVF-----CHIGVLDKDLFEYKRGGRNNVNDLKQAFYRF 225
DB 225 MRFETLPPFMALVPPYLMNRSPOKQSH--YHPDSDLFPRK-----KKDY 268
OY 226 LQTYVYHOLA--LIALLYVG-----GPPYIWMGGRFLVMEFSTRAINSVCHK- 274
DB 269 LSTNCKRTMALLVCLNFVGPRTOMLKLYGIPYIEFMMWLDLYLH-----HHG 319
OY 275 -----WGRFPMN--TGDLSTNNMFVALCAFGEGMHN-----HHAFGSARHG 315
DB 320 HEDKLPWYRGKMSYLRGLTLTDR-----DYGMINNIHHDGTHVHILFQIPHYH 372
OY 316 L 316
DB 373 L 373

```

Search completed: September 13, 2002, 11:58:48
Job time: 7764 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 13, 2002, 09:47:44 : Search time 68.94 Seconds
(without alignments)
893.330 Million cell updates/sec

Title: US-09-664-840-2
1946
Sequence: 1 LRLSLVPPISISLSLEAM.....ATNKLPLEAKOKLAKSA 356

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organella:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*
15: SP-virus:*
16: SP-bacteriap:*
17: SP-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1940	99.7	356	10	Q9FV68 Limanthus
2	978.5	50.3	371	10	Q9LVZ4 Arabidopsis
3	976.5	50.2	371	10	Q949X0 Arabidopsis
4	887.5	45.6	305	10	Q65797 Arabidopsis
5	874.5	44.9	307	10	Q65798 Arabidopsis
6	870.5	44.7	311	10	Q9SID2 Arabidopsis
7	833	42.8	299	10	Q9LND8 Arabidopsis
8	801	41.2	303	10	Q04700 Arabidopsis
9	796	40.9	314	10	Q9LVZ3 Arabidopsis
10	792	40.7	299	10	Q9FVZ3 Arabidopsis
11	788.5	40.5	319	10	Q9LMI4 Arabidopsis
12	786.5	40.4	299	10	Q9LMI3 Arabidopsis
13	775.5	39.9	299	10	Q9LND9 Arabidopsis
14	741	38.1	287	10	Q9LND6 Arabidopsis
15	687	35.3	272	2	Q44502 Arabidopsis
16	650	33.4	318	16	Q55406 Arabidopsis

17	632.5	32.5	270	2	Q33722 Arabidopsis
18	626	32.2	277	2	Q07873 Arabidopsis
19	595	30.6	279	2	Q9ZAP7 Arabidopsis
20	556	28.6	278	2	Q44117 Arabidopsis
21	448	23.0	300	2	Q9R6T6 Arabidopsis
22	445	22.9	336	2	Q9K3T6 Arabidopsis
23	423.5	21.8	479	3	Q94523 Arabidopsis
24	407	20.9	555	3	P79078 Arabidopsis
25	402	20.7	493	3	P79077 Arabidopsis
26	384.5	19.8	292	5	Q94824 Arabidopsis
27	369	19.0	476	10	Q80331 Arabidopsis
28	366.5	18.8	384	5	Q9VFX5 Arabidopsis
29	362	18.6	452	3	Q13378 Arabidopsis
30	359.5	18.5	461	5	Q9VAG9 Arabidopsis
31	359	18.4	451	3	P79049 Arabidopsis
32	358.5	18.4	339	5	Q01708 Arabidopsis
33	357.5	18.4	445	3	Q94215 Arabidopsis
34	355	18.2	445	3	Q9VW5 Arabidopsis
35	354	18.2	445	3	Q94214 Arabidopsis
36	354	18.2	445	3	Q94747 Arabidopsis
37	352.5	18.1	383	5	Q94541 Arabidopsis
38	352	18.1	324	13	Q9PW15 Arabidopsis
39	352	18.1	486	3	Q94036 Arabidopsis
40	351.5	18.1	383	5	Q9VC66 Arabidopsis
41	350.5	18.0	292	5	Q15810 Arabidopsis
42	350.5	18.0	383	5	Q9U967 Arabidopsis
43	349.5	18.0	351	5	Q9NG08 Arabidopsis
44	349	17.9	355	11	Q92216 Arabidopsis
45	348.5	17.9	383	5	Q9U972 Arabidopsis

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	356 AA.
Q9FV68	Q9FV68	Q9FV68		
AC	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	DELTA5 ACYL-CoA DESATURASE (FRAGMENT).			
OS	Limanthus douglasii (Douglas's meadowfoam).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eurosid II; Brassicales; Limnathaceae; Limnathes.			
OX	NCBI_TaxId=28973;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20438218; PubMed=10982439;			
RA	Cahoon E.B., Marillia E.F., Stecca K.L., Hall S.E., Taylor D.C.,			
RA	Kliney A.J.;			
RT	"Production of fatty acid components of meadowfoam oil in somatic			
RT	soybean embryos."			
RL	Plant Physiol. 124:243-252(2000).			
DR	EMBL; AF247133; AAC28599.1; -.			
DR	InterPro: IPR001522; Desaturase.			
DR	Pfam: PF01069; Desaturase: 1.			
DR	PRINTS: PR00075; FACSATSATASE.			
DR	ProDom: PD002221; Desaturase: 1.			
FT	NON-TER			
SQ	SEQUENCE 356 AA; 41038 MW; E0CD4BCB8F7B534C CRC64;			

Query Match 99.7%: Score 1940; DB 10; Length 356;
Best Local Similarity 99.4%: Pred. No. 5.2e-176;
Matches 354; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY	1	LRLSLVPPISISLSLEAMSFATTPAMPFASVLDPKRTKPEKTRPKDDLE 60
DB	1	LRLSLVPPISISLSLEAMSFATTPAMPFASVLDPKRTKPEKTRPKDDLE 60
OY	61	RFTSEVLEKSKGFMRRKMPDIONAVTLVLVLAAMAPPYFSWDAFWISFILGP 120

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Db 61 RFRSEVLERAKGFMRRKMPRIQNAVTLVLAALAAAPFESWDAFWISILLGF 120
Qy 121 ASGVGLITLCHRCCLTHGFGFLPKLYEFPAFCGSLALOGDPMENSHNRHNOVDTER 180
Db 121 ASGVGLITLCHRCCLTHGFGFLPKLYEFPAFCGSLALOGDPMENSHNRHNOVDTER 180
Qy 181 DVHSEPTGFMFCGHWLVDKDLFEYKRGGRNNVNDLKKQAFYRFLQTYMHQALIAL 240
Db 181 DVHSEPTGFMFCGHWLVDKDLFEYKRGGRNNVNDLKKQAFYRFLQTYMHQALIAL 240
Qy 241 LYYGGEFYIYMGWGFRLVFMHSEFALNSVCHKMGGRPMNTGDLSTNNMFALCAFGEG 300
Db 241 LYYGGEFYIYMGWGFRLVFMHSEFALNSVCHKMGGRPMNTGDLSTNNMFALCAFGEG 300
Qy 301 WHNNHAFEGSARHGLEWMOIDTWYVIRTLQALIGLATNVKLPTEAKOKKLAKSA 356
Db 301 WHNNHAFEGSARHGLEWMOIDTWYVIRTLQALIGLATNVKLPTEAKOKKLAKSA 356
```

```
RESULT 2
Q9LVZ4 PRELIMINARY; PRT; 371 AA.
ID 09LVZ4
AC 09LVZ4
DT 01-OCT-2000 (TREMBLREL. 15, Created)
DT 01-OCT-2000 (TREMBLREL. 15, Last sequence update)
DE DELTA 9 DESATURASE- LIKE PROTEIN.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA.
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA.
RA MEDLINE-20277480; PubMed-10819329;
RX Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty p1 and TAC
RT clones.";
RL DNA Res. 7:131-135(2000).
EMBL: AB017071; BAB02316.1; -.
DR InterPro: IPR001522; Desaturase.
DR Pfam: PF01069; Desaturase.1.
DR PRINTS: PR00075; FACDDSATRASE.
DR PRODOM: PD002221; Desaturase; 1.
SQ SEQUENCE 371 AA; 42580 MW; F1D62B9F44795FCC CRC64;
```

Query Match 50.38; Score 978.5; DB 10; Length 371;
Best Local Similarity 56.28; Pred. No. 1.1e-84;
Matches 173; Conservative 52; Mismatches 80; Indels 3; Gaps 3;

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Qy 45 KPEKTEPRKDKDLERFRSEVLERKSK-GFMRKKNPRDIONAVTLVLAALAAAP 103
Db 61 KRDTTAAATGEGYRRIMLSDVLYKKKEKYWWEKKAADFCAVAVVLSMHLSTLAP 120
Qy 104 EYFSMDAFWISFILLGFASGVGLITLCHRCCLTHGFGFLPKLYEFPAFCGSLALOGDPM 163
Db 121 FQFMRAVAVAFGLY-ITVGLIGLITLSFHRNLSHKAFLPKWLELYLFAVCGAQAALQGNPI 179
Qy 164 EYWSNHRHNOFVDTERDVHSEPTGFMFCGHWLVDKDLFEYKRGGRNNVNDLKKQAFY 223
Db 180 DVHSEPTGFMFCGHWLVDKDLFEYKRGGRNNVNDLKKQAFY 223
Qy 224 RFLQKTYMHQALIALYYGGEFYIYMGWGFRLVFMHSEFALNSVCHKMGGRPMNTG 283
Db 241 LYYGGEFYIYMGWGFRLVFMHSEFALNSVCHKMGGRPMNTG 283
```

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Db 239 RFLRTTYLHPLALAVALYAMGFEFYIYMGWGFRLVFMHSEFALNSVCHKMGGRPMNTG 298
Qy 284 DLSTNNMFALCAFGEGWHNNHAFEGSARHGLEWMOIDTWYVIRTLQALIGLATNVKLP 343
Db 299 DLSTNNMFALCAFGEGWHNNHAFEGSARHGLEWMOIDTWYVIRTLQALIGLATNVKLP 358
Qy 344 TEAKOKKL 351
Db 359 SEAKOKRM 366
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```
RESULT 3
Q949X0 PRELIMINARY; PRT; 371 AA.
ID 0949X0
AC 0949X0
DT 01-DEC-2001 (TREMBLREL. 19, Created)
DT 01-DEC-2001 (TREMBLREL. 19, Last sequence update)
DE DELTA 9 DESATURASE.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M.,
RA Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L.,
RA Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L.,
RA Carinci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamliya A., Karlin-Neuman G., Kawai J., Kim C., Koeseema E., Lam B.,
RA Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Sakurai T., Satou M., Seki M., Shim P., Southwick A., Tracy S.E.,
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "Full length cDNA of gene MSU1.25/AT3G15850 (GI:11994357).";
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY050838; AAK92773.1; -.
SQ SEQUENCE 371 AA; 42550 MW; 45C67AD60CE1860D CRC64;
```

Query Match 50.28; Score 976.5; DB 10; Length 371;
Best Local Similarity 56.28; Pred. No. 1.7e-84;
Matches 173; Conservative 52; Mismatches 80; Indels 3; Gaps 3;

```
Qy 45 KPEKTEPRKDKDLERFRSEVLERKSK-GFMRKKNPRDIONAVTLVLAALAAAP 103
Db 61 KRDTTAAATGEGYRRIMLSDVLYKKKEKYWWEKKAADFCAVAVVLSMHLSTLAP 120
Qy 104 EYFSMDAFWISFILLGFASGVGLITLCHRCCLTHGFGFLPKLYEFPAFCGSLALOGDPM 163
Db 121 FQFMRAVAVAFGLY-ITVGLIGLITLSFHRNLSHKAFLPKWLELYLFAVCGAQAALQGNPI 179
Qy 164 EYWSNHRHNOFVDTERDVHSEPTGFMFCGHWLVDKDLFEYKRGGRNNVNDLKKQAFY 223
Db 180 DVHSEPTGFMFCGHWLVDKDLFEYKRGGRNNVNDLKKQAFY 223
Qy 224 RFLQKTYMHQALIALYYGGEFYIYMGWGFRLVFMHSEFALNSVCHKMGGRPMNTG 283
Db 239 RFLRTTYLHPLALAVALYAMGFEFYIYMGWGFRLVFMHSEFALNSVCHKMGGRPMNTG 298
Qy 284 DLSTNNMFALCAFGEGWHNNHAFEGSARHGLEWMOIDTWYVIRTLQALIGLATNVKLP 343
Db 299 DLSTNNMFALCAFGEGWHNNHAFEGSARHGLEWMOIDTWYVIRTLQALIGLATNVKLP 358
Qy 344 TEAKOKKL 351
Db 359 SEAKOKRM 366
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RESULT 4
ID 065797 PRELIMINARY; PRT; 305 AA.
AC 065797;

QY 294 LCAGEGHHNNHAFESARHGLEWMOIDVTWYVIRTLQALGATNVKLPTEAOKKL 351
 DB 238 PFTMGESHHNNHAFESARHGLEWMOIDVTWYVIRTLQALGATNVKLPTEAOKRKM 295

RESULT 11

Q9LMT4 PRELIMINARY; PRT; 319 AA.

AC Q9LMT4; 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
 DE 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE T2D23.5 PROTEIN.
 GN T2D23.5.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 CX NCBL_TaxID=3702;

RA SEQUENCE FROM N.A.
 RC STRAIN=CV, COLUMBIA;
 RA Liu S.X., Vaysberg M., Etgu P., Lee J.M., Lenz C., Pham P., Sakano H.,
 Toriumi M., Yu G., Chan A., Chung M., Goldsmith A., Liu A., Smith A.,
 Altafi H., Brooks S., Buehler E., Chao Q., Conn L., Conway A.B.,
 Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M.,
 Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R.,
 Federici N.A., Theologis A.;
 RA "The sequence of BAC T2D23 from Arabidopsis thaliana chromosome 1.";
 RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AC068143; AF82163.1; -
 DR InterPro: IPR001522; Desaturase.
 DR Pfam: PF01069; Desaturase; 1.
 DR PRINTS: PR00075; FACDDSATRASE.
 DR ProDom: PD002221; Desaturase; 1.
 SQ SEQUENCE 319 AA; 37455 MW; 82377E95153550A2 CRC64;

Query Match 40.5%; Score 788.5; DB 10; Length 319;
 Best Local Similarity 50.2%; Pred. No. 1e-66;
 Matches 144; Conservative 46; Mismatches 94; Indels 3; Gaps 2;

QY 65 SEVLEKSKGFWRKRNPRDIONAVTLVLAALAAAFYFSDAWISFLLGFASGV 124
 DB 32 SRVYSTQKRAVYFORQPLVDVYVAVYVHFLCLAPFNKWEA--LRGLVIFALTT 89
 QY 125 LGILCFHRCILTHGGFKLPKLYEFYFVAVCGSLAGDPMEMVSNHRYHNOVDTERVHS 184
 DB 90 LSTFSEHRLNLSHSEFKIPKLETPMAVSAYFAVLAQGDPMVSIHRFHQFTDSDRDPHS 149
 QY 185 PTOGFWECHIGWLDKDLFEKRGGRNNVNDLKKQAFYRFLQKTYMHQALALALYYV 244
 DB 150 PKEGILSHLIMIFDQYIKKCGG-RDNVLDLKKQWFKYKRLRTIAVHILMEFTIILY 208
 QY 245 GGFYIWMGKFLVFMFHSFAINSVCHKMGKRPWNTGDLSTNNMFVALLCAFGEGHHNN 304
 DB 209 GGLPYLTCGGVGVGIFIGYHVTWLVNSACHIMGSRSWTKDTSRRVWMLSTFTMGESHHNN 268
 QY 305 HHAFESARHGLEWMOIDVTWYVIRTLQALGATNVKLPTEAOKKL 351
 DB 269 HHAFESARHGLEWMOIDVTWYVIRTLQALGATNVKLPTEAOKRKM 315

RESULT 12

Q9LMT3 PRELIMINARY; PRT; 299 AA.

AC Q9LMT3; 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
 DE 01-JUN-2001 (Tremblrel. 17, last annotation update)
 DE T2D23.6 PROTEIN (PUTATIVE DELTA 9 DESATURASE PROTEIN).
 GN T2D23.6.
 OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 CX NCBL_TaxID=3702;

RA SEQUENCE FROM N.A.
 RC STRAIN=CV, COLUMBIA;
 RA Liu S.X., Vaysberg M., Etgu P., Lee J.M., Lenz C., Pham P., Sakano H.,
 Toriumi M., Yu G., Chan A., Chung M., Goldsmith A., Liu A., Smith A.,
 Altafi H., Brooks S., Buehler E., Chao Q., Conn L., Conway A.B.,
 Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M.,
 Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R.,
 Federici N.A., Theologis A.;
 RA "The sequence of BAC T2D23 from Arabidopsis thaliana chromosome 1.";
 RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [12]

RA SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Etgu P., Lee J.M.,
 Toriumi M., Yu G., Brooks S., Chao Q., Chen H., Karlin-Neumann G.,
 Kim C., Lam B., Miranda M., Nguyen M., Palm C.J., Shinn P.,
 Southwick A., Davis R.W., Ecker J.R., Theologis A.;
 RT "Full length cDNA of gene T2D23.6 (GI:8927673).";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC068143; AF82164.1; -
 DR EMBL; AF332427; AA648790.1; -
 DR InterPro: IPR001522; Desaturase.
 DR Pfam: PF01069; Desaturase; 1.
 DR PRINTS: PR00075; FACDDSATRASE.
 DR ProDom: PD002221; Desaturase; 1.
 SQ SEQUENCE 299 AA; 35510 MW; 9682DBF5BA46E35D CRC64;

Query Match 40.4%; Score 786.5; DB 10; Length 299;
 Best Local Similarity 50.5%; Pred. No. 1.e-66;
 Matches 143; Conservative 42; Mismatches 95; Indels 3; Gaps 2;

QY 69 LEKSKGFWRKRNPRDIONAVTLVLAALAAAFYFSDAWISFLLGFASGVGIT 128
 DB 16 VSKKRPYIHREMSWADIIRALTYINVHFLCLAPFNKWEALRFGVLAVALS--LST 73
 QY 129 LCFHRCILTHGGFKLPKLYEFYFVAVCGSLAGDPMEMVSNHRYHNOVDTERVHSPTG 188
 DB 74 FSYHRLNLSHSEFKIPKLETPMAVSAYFAVLAQGDPLDWVSIHRFHQFTDSDRDPHSIEG 133
 QY 189 FWFCHIGWLDKDLFEKRGGRNNVNDLKKQAFYRFLQKTYMHQALALALYYVGF 248
 DB 134 FWEHVMICDTRIKYKCGG-RNNVMDLKKQWFKYKRLRTIAVHILMEFTIILYGLP 192
 QY 249 YIWMGKFLVFMFHSFAINSVCHKMGKRPWNTGDLSTNNMFVALLCAFGEGHHNNHAF 308
 DB 193 YLTCGGVGVGIVYHVTWLVNSACHIMGSRSWTKDTSRRVWMLSTFTMGESHHNNHAF 252
 QY 309 EGSARHGLEWMOIDVTWYVIRTLQALGATNVKLPTEAOKKL 351
 DB 253 ESSARHGLEWMOIDVTWYVIRTLQALGATNVKLPTEAOKRKL 295

RESULT 13

Q9LND9 PRELIMINARY; PRT; 299 AA.

AC Q9LND9; 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
 DE 01-JUN-2001 (Tremblrel. 17, last annotation update)
 DE T2IE18.14 PROTEIN.
 GN T2IE18.14.
 OS Arabidopsis thaliana (Mouse-ear cress).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 CX NCBL_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-CV, COLUMBIA:
 RA Sakano H., Vayenberg M., Lee J., Lenz C., Liu S.X., Pham P.,
 RA Tortum M., Yu G., Chin C., Chlou J., Choi E., Chung M., Gonzalez A.,
 RA Hong B., Liu A., Altai H., Brooks S., Buehler E., Chao Q., Conn L.,
 RA Conway A.B., Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B.,
 RA Miranda M., Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W.,
 RA Ecker J.R., Federpsel N.A., Theologis A.;
 RT "The sequence of BAC T21E18 from Arabidopsis thaliana chromosome 1.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC024174; AAF80132.1; -
 DR InterPro: IPR001522; Desaturase.
 DR Pfam: PF01069; Desaturase; 1.
 DR PRINTS: PR00075; FACDSATURASE.
 DR ProDom: PD002221; Desaturase; 1.
 SQ SEQUENCE 299 AA; 34769 MW; 4640982a38CA9E46 CRC64;

Query Match 39.9%; Score 775.5; DB 10; Length 299;
 Best Local Similarity 51.8%; Pred. No. 1.6e-65;
 Matches 145; Conservative 37; Mismatches 95; Indels 3; Gaps 2;

OY 72 KSKFMRKRNPRDIONAVTLVLAALANAPFEYSMDAFWISFLLGFASGVLTICP 131
 DB 19 EKRAFEFRKTRIDIAASAVGAVHLCLLAFENYKWEALRFGVILATVTS--LSITFSY 76
 OY 132 HRCITGGFKLPKLYEYFAVCGSLAGDPMENVNHRHYHQFVDERVHSPTQGFWR 191
 DB 77 HNRITHSFKLPKLEFPFAVSALFALQGHPTDWSVTHRHQPTSDRPHSPTGCFWR 136
 OY 192 CHIGWVLDKDLFEKRGRRNNVNDLKKQAFYRFLOKTYMHOLALIALIYYGGFPYIV 251
 DB 137 SHVFWIDTSTYIREKCGG-RDNVMDLQKQWEYRFLRNTIGLITLTWLVLYMGDLYLR 195
 OY 252 MCGMFRLVFHFSTFALNSCHMGCGRPWNTGDLSTNNMVALCAGEGHHNNHAFEOS 311
 DB 196 CGVGVGGTITVNGTGLNSCHMGCGRPWNTGDLSTNNMVALCAGEGHHNNHAFEOS 255
 OY 312 ARHGLEWQIDVTWYVIRTLQAIGLATVNLPTGAOKRL 351
 DB 256 ARHGLEWQIDVTWYVIRTLQAIGLATVNLPTGAOKRL 295

RESULT 14
 ID 09LND6 PRELIMINARY; PRT; 287 AA.
 AC 09LND6;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE T21E18.17 PROTEIN.
 GN T21E18.17.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucotyle II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV, COLUMBIA;
 RA Sakano H., Vayenberg M., Lee J., Lenz C., Liu S.X., Pham P.,
 RA Tortum M., Yu G., Chin C., Chlou J., Choi E., Chung M., Gonzalez A.,
 RA Hong B., Liu A., Altai H., Brooks S., Buehler E., Chao Q., Conn L.,
 RA Conway A.B., Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B.,
 RA Miranda M., Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W.,
 RA Ecker J.R., Federpsel N.A., Theologis A.;
 RT "The sequence of BAC T21E18 from Arabidopsis thaliana chromosome 1.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC024174; AAF80132.1; -
 DR InterPro: IPR001522; Desaturase.
 DR Pfam: PF01069; Desaturase; 1.
 DR PRINTS: PR00075; FACDSATURASE.
 DR ProDom: PD002221; Desaturase; 1.
 SQ SEQUENCE 287 AA; 33565 MW; 6F491EF973F6201F CRC64;

Query Match 38.1%; Score 741; DB 10; Length 287;
 Best Local Similarity 47.0%; Pred. No. 2.9e-62;
 Matches 140; Conservative 44; Mismatches 96; Indels 18; Gaps 5;

OY 54 KPRDLEFRSTSEVLEKSKGFMRRKRNPRDIONAVTLVLAALANAPFEYSMDAFWI 113
 DB 4 KNRDSS---SQKAVRKKERAFLEFRKTRVDYMRASAVGAVHLCLLAFENYKWEALRFGVILATVTS--LSITFSY 76
 OY 114 SFLLGFASGVLTICFHRCLTHGFGPKLPKLYEYFAVCGSLAGDPMENVNHRHYHQFVDERVHSPTQGFWR 173
 DB 61 A-AMVISTN-LSITFSYHNRHLSRFSKLPKLEYPFAVSALFALQGHPTDWSVTHRHQPTSDRPHSPTGCFWR 118
 OY 174 QFVDTEDVSPQGFHGFICGVLDKDLFEKRGRRNNVNDLKKQAFYRFLOKTYMHOLALIALIYYGGFPYIV 233
 DB 119 QFTDSDRPHSPTGCFHGFICGVLDKDLFEKRGRRNNVNDLKKQAFYRFLOKTYMHOLALIALIYYGGFPYIV 177
 OY 234 QALIALIYYGGFPYIVMGFRLVFHFSTFALNSCHMGCGRPWNTGDLSTNNMVALCAGEGHHNNHAFEOS 293
 DB 178 ILTFWLVLYMGDLYLRITLQSVGALGYHATWLINSACHINGSRANNMTKTSRNIMWILG 237
 OY 294 LCAFEGSHNNHAFEOSARHGLEWQIDVTWYVIRTLQAIGLATVNLPTGAOKRL 351
 DB 238 PFTMGESMNNHAFEOSARHGLEWQY-----LGLATDVKLPTDAOKRM 283

RESULT 15
 ID 044502 PRELIMINARY; PRT; 272 AA.
 AC 044502;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE FATVY-ACID DESATURASE.
 GN DESC.
 OS Anabaena variabilis.
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
 OC NCBI_TaxID=1172;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95014360; PubMed=7929259;
 RA Sakamoto T., Wada H., Nishida I., Omori M., Murata N.;
 RT "Delta 9 acyl-lipid desaturases of cyanobacteria. Molecular cloning
 RT and substrate specificities in terms of fatty acids, sn-positions, and
 RT polar head groups.";
 RL J. Biol. Chem. 269:25576-25580(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94207189; PubMed=8155883;
 RA Sakamoto T., Wada H., Nishida I., Omori M., Murata N.;
 RT "Identification of conserved domains in the delta 12 desaturases of
 RT cyanobacteria.";
 RL Plant Mol. Biol. 24:643-650(1994).
 DR EMBL: D14581; BAA03434.1; -
 DR InterPro: IPR001522; Desaturase.
 DR Pfam: PF01069; Desaturase; 1.
 DR PRINTS: PR00075; FACDSATURASE.
 DR ProDom: PD002221; Desaturase; 1.
 SQ SEQUENCE 272 AA; 31418 MW; E2FBD0CB49D0D0656 CRC64;

Query Match 35.3%; Score 687; DB 2; Length 272;
 Best Local Similarity 47.6%; Pred. No. 3.7e-57;
 Matches 128; Conservative 48; Mismatches 73; Indels 20; Gaps 4;

OY 88 NAVTLVLA--ALANAPFEYSMDAFWISFLLGFASGVLTICFHRCLTHGFGPKLPK 145
 DB 15 NTLFGLHIALALPAFLPSNFSMAAVGA-LLLVWITGGLGITLGFRLVTHRSFQTPKW 73
 OY 146 VEYFAVCGSLAGDPMENVNHRHYHQFVDERVHSPTQGFHGFICGVLT----- 198
 DB 74 LEYFLVLCGLTACGGGLEWVGTIRIHLSHSDTDPDPDHDSNKGKFWMSHIGMLIYHSFSA 133

